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Access DB# 109419

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Air Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, author, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 = 703-308-4498
ian.delaval@uspto.gov

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Searcher	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	SA Sequence (#) _____	STN _____
Searcher Phone # <u>4498</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel Orbit _____
Date Request Received <u>12/12</u>	Bibliographic _____	Dr. Link _____
Date Completed <u>12/12</u>	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Client Prep Time <u>15</u>	Patent Family _____	WWW Internet _____
Fee <u>\$10</u>	Other _____	Other (specify) _____
PT _____		



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109419

TO: Phillip Gambel
Location: 8b13 / 9e12
Tuesday, December 02, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 772103

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

STIC
01/02/2004
Biotech-Chem Library
01/02/2004
jan.delaval@uspto.gov

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:39:15 ; Search time 15.8316 Seconds

(without alignments)
1354.605 Million cell updates/sec

Title: US-09-772-103-2

Sequence: 1174

1 MACLGFORHKAQNLATRTM.....MPPTPECEKQOPFIPIN 223

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 76: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159	98.7	223	2	cytotoxic T-lympho
2	997	84.9	223	2	CTLA-4 precursor
3	970	82.6	186	2	cytotoxic T-lympho
4	878	74.8	223	2	cytotoxic T-lympho
5	211	18.0	221	2	CD28 protein - ch
6	204	17.4	221	2	CD28 precursor - r
7	200	17.0	36	2	cytotoxic T-lympho
8	187	15.9	220	1	CD28 precursor - r
9	174.5	14.9	173	2	cytotoxic T-lympho
10	170	14.5	218	2	cell surface gly
11	158	13.5	218	2	cell surface gly
12	101	8.6	132	2	cell surface gly
13	100.5	8.6	124	2	cell surface gly
14	99	8.4	124	2	cell surface gly
15	97	8.3	108	2	cell surface gly
16	97	8.3	108	2	cell surface gly
17	94	8.0	117	2	cell surface gly
18	93	7.9	117	2	cell surface gly
19	92	7.8	117	2	cell surface gly
20	91	7.8	108	2	cell surface gly
21	91	7.8	108	2	cell surface gly
22	90.5	7.7	108	2	cell surface gly
23	90.5	7.7	123	2	cell surface gly
24	90	7.7	140	2	cell surface gly
25	89.5	7.6	3707	2	cell surface gly
26	89	7.6	125	2	cell surface gly
27	88	7.5	573	2	cell surface gly
28	87.5	7.5	88	2	cell surface gly
29	87.5	7.5	213	2	cell surface gly

30	87	7.4	207	2	150609	T-cell surface gly
31	87	7.4	739	2	JS0675	vascular cell adhe
32	86	7.3	120	2	S30525	ig lambda chain v
33	86	7.3	125	2	S40349	ig kappa chain v-j
34	86	7.3	199	2	S78540	inducible t-cell c
35	86	7.3	224	2	S14237	ig kappa chain pre
36	86	7.3	739	2	UN0581	vascular cell adhe
37	85.5	7.3	598	2	T42070	protein serine/thr
38	85	7.2	111	2	S36281	ig lambda chain v
39	85	7.2	112	2	PL0274	ig kappa chain v r
40	85	7.2	125	2	S40333	ig kappa chain v-j
41	85	7.2	1367	2	A4128	protein-tyrosine k
42	84.5	7.2	105	2	S26338	ig kappa chain v r
43	84.5	7.2	124	2	S40318	ig kappa chain v r
44	84	7.2	111	2	S38497	ig lambda chain -
45	84	7.2	112	2	H26317	ig kappa chain v r

ALIGNMENTS

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T09536
J/Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
R/Immunol. 147, 1037-1044, 1991
A/Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mo
A/Reference number: 149584; MUID:91318145; PMID:1713603
A/Accession: T09536
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-223 <HAR>
A/Cross-references: EMBL:U15006; NID:g291928; PIDN:AAB59385.1; PID:g291929
C/Genetics:
A/Map position: 2q33
C/Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C/Keywords: T-cell; transmembrane protein

Query Match 98.7%; Score 1159; DB 2; Length 223;
Best Local Similarity 98.7%; Pred. No. 7.2e-100;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTMPTCLLFFLLFVPCAMVAVPAVAVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQNLATRTMPTCLLFFLLFVPCAMVAVPAVAVLASSRGIAFVCEY 60
QY 61 ABRGKATRYVTVLRQADSOVTEVCATYTMGNELTFDDSICTGSSGNQNLITQGR 120
DB 61 ABRGKATRYVTVLRQADSOVTEVCATYTMGNELTFDDSICTGSSGNQNLITQGR 120
QY 121 AMDTGLYICKVLMAPPYVYLGIGNAQIYVIDPECPDSDFLMLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVLMAPPYVYLGIGNAQIYVIDPECPDSDFLMLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPPTPECEKQOPFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPPTPECEKQOPFIPIN 223

RESULT 2

I46696

CTLA-4 precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C/Accession: I46696
R/Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A/Reference number: I46689; MUID:95369849; PMID:7642234

A:Accession: 146696
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-223 <ISO>
 A:Cross-references: GB:149844; NID:g755100; PIDN:BA08644.1; PID:g755101
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match 84.9%; Score 997; DB 2; Length 223;
 Best Local Similarity 84.3%; Pred. No. 7,1e-85;

Matches 188; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCITLFLFIPFCKAMHVAQPAVLASSRGIAFPVCEY 60
 DB 1 MARLGFQROCTQDLASRTWSCALFSLFLPVSFKLHVSPAVVLASSRGVAFVCEY 60
 QY 61 ASGKATREVVTVLRQADSOVTEVCATVMNGNELFLDLSICTGSSGNQVNLITQGR 120
 DB 61 ASHKAIEVVTVLRLQANSQTEVCANTYVENELTFIDSTCTGISHGKVLITQGLS 120
 QY 121 AMDTGLYICKVELMPPPYLYGNGAQIYVIDPEPCPSDFLMLIAAVSSGLFFYSFL 180
 DB 121 AMDTGLYICKVELMPPPYLYGNGAQIYVIDPEPCPSDFLMLIAAVSSGLFFYSFL 180
 QY 181 LTVAVSLSKMLKKRSPLTTGGVYVKKMPTEPECKQOPFYFIPIN 223
 DB 181 ITAVSLSKMLKKRSPLTTGGVYVKKMPTEPECKQOPFYFIPIN 223

RESULT 3

S08614
 cytotoxic T-lymphocyte protein 4 - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
 C:Accession: S08614

R:Barlavan, P.; Mattei, M.G.; Golstein, P.; Lefranc, M.P.
 Eur. J. Immunol. 18, 1901-1905, 1988

A:Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of pro
 A:Reference number: S08614; MUID:89120925; PMID:3220103

A:Accession: S08614
 A:Molecule type: DNA

A:Residues: 1-186 <DAR>
 A:Cross-references: EMBL:X15070; NID:g30283; PID:g825649
 C:Genetics:

A:Gene: GDB:CTLA4

A:Cross-references: GDB:119818; OMIM:123890
 A:Map position: 2q33-2q33

A:Introns: 116/1; 152/3

C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

F:125-150/Domain: transmembrane #status predicted <TMM>
 F:151-186/Domain: intracellular #status predicted <INT>
 F:21-92/Disulfide bonds: #status predicted

Query Match 82.6%; Score 970; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.8e-82;

Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 MHVAQPAVLASSRGIAFPVCEYASRGKATREVVTVLRQADSOVTEVCATVMNGNELTF 97
 DB 1 MHVAQPAVLASSRGIAFPVCEYASRGKATREVVTVLRQADSOVTEVCATVMNGNELTF 60
 QY 98 LDDSICTGSSGNQVNLITQGRAMDGLYICKVELMPPPYLYGNGAQIYVIDPEPC 157
 DB 61 LDDSICTGSSGNQVNLITQGRAMDGLYICKVELMPPPYLYGNGAQIYVIDPEPC 120
 QY 158 PSDSFLMLIAAVSSGLFFYSFLITAVSLSKMLKKRSPLTTGGVYVKKMPTEPECKQOP 217
 DB 121 PSDSFLMLIAAVSSGLFFYSFLITAVSLSKMLKKRSPLTTGGVYVKKMPTEPECKQOP 180
 QY 218 YFIPIN 223
 DB 181 YFIPIN 186

RESULT 4

A29063

cytotoxic T-lymphocyte protein 4 - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
 C:Accession: A29063; 149622

R:Brinnet, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.;
 Nature 328, 267-270, 1987

A:Title: A new member of the immunoglobulin superfamily--CTLA-4.
 A:Reference number: A29063; MUID:87258259; PMID:3496540

A:Accession: A29063
 A:Molecule type: mRNA

A:Residues: 1-223 <BRU>
 A:Cross-references: GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593

R:Harper, K.; Balzano, C.; Kourlier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
 J. Immunol. 147, 1037-1044, 1991

A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mou
 A:Reference number: 149584; MUID:91318145; PMID:1713603

A:Accession: 149622
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-36 <RES>
 A:Cross-references: GB:M74362; NID:g192833; PIDN:AAA7489.1; PID:g553903

C:Genetics:
 A:Gene: CTLA-4

A:Map position: 1, band C
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match 74.8%; Score 878; DB 2; Length 223;
 Best Local Similarity 74.0%; Pred. No. 7.4e-74;

Matches 165; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCITLFLFIPFCKAMHVAQPAVLASSRGIAFPVCEY 60
 DB 1 MACLGFORHKAQNLATRTWPCITLFLFIPFCKAMHVAQPAVLASSRGIAFPVCEY 60
 QY 61 ASGKATREVVTVLRQADSOVTEVCATVMNGNELFLDLSICTGSSGNQVNLITQGR 120
 DB 61 ASGKATREVVTVLRQADSOVTEVCATVMNGNELFLDLSICTGSSGNQVNLITQGR 120
 QY 121 AMDTGLYICKVELMPPPYLYGNGAQIYVIDPEPCPSDFLMLIAAVSSGLFFYSFL 180
 DB 121 AMDTGLYICKVELMPPPYLYGNGAQIYVIDPEPCPSDFLMLIAAVSSGLFFYSFL 180
 QY 181 LTVAVSLSKMLKKRSPLTTGGVYVKKMPTEPECKQOPFYFIPIN 223
 DB 181 VSAVSLSKMLKKRSPLTTGGVYVKKMPTEPECKQOPFYFIPIN 223

RESULT 5

S25168

CHT28 protein - chicken
 C:Species: Gallus gallus (chicken)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: I50619; S25168

R:Young, J.R.; Davidson, T.F.; Tregaskes, C.A.; Rennie, M.C.; Vainio, O.
 J. Immunol. 152, 3848-3851, 1994

A:Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
 A:Reference number: I50619; MUID:94194147; PMID:8144954

A:Accession: I50619
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-221 <Y02>

A:Cross-references: EMBL:X67915; NID:g63221; PIDN:CAA48114.1; PID:g63222
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match 18.0%; Score 211; DB 2; Length 221;
 Best Local Similarity 31.5%; Pred. No. 4.1e-12;
 Matches 67; Conservative 36; Mismatches 88; Indels 22; Gaps 10;

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:49 ; Search time 10.4037 Seconds
(without alignments)
1008.007 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 MACLCFORHQAQLNATRTM.....MPTEPECKQKQPPYFIPIN 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1170	99.7	223	1	CTLA4_HUMAN
2	1010	86.0	223	1	CTLA4_PIG
3	997	84.9	223	1	CTLA4_RABIT
4	878	74.8	223	1	CTLA4_MOUSE
5	211	18.0	221	1	CD28_CHICK
6	204	17.4	221	1	CD28_RABIT
7	203	17.3	219	1	CD28_BOVIN
8	187	15.9	220	1	CD28_HUMAN
9	170	14.5	218	1	CD28_MOUSE
10	156	13.3	218	1	CD28_RAT
11	93	7.9	301	1	NADA_CLOPE
12	91	7.8	4391	1	PGEM_HUMAN
13	89.5	7.6	3707	1	PGEM_MOUSE
14	87	7.4	739	1	VCAI_RAT
15	86	7.3	739	1	VCAI_MOUSE
16	85	7.2	1356	1	VGR2_HUMAN
17	85	7.2	1367	1	VGR2_MOUSE
18	84	7.2	480	1	SAHH_XANPC
19	83	7.1	111	1	LV2A_HUMAN
20	83	7.1	111	1	LV2D_HUMAN
21	83	7.1	1343	1	CI82_RAT
22	82	7.0	215	1	CI82_HUMAN
23	81.5	6.9	111	1	KV12_RABIT
24	81.5	6.9	1897	1	PTPF_HUMAN
25	81	6.9	246	1	MOG_MOUSE
26	80.5	6.9	568	1	PHAC_CHRYO
27	80.5	6.9	715	1	LOC1_LACIA
28	79.5	6.8	108	1	KV6K_MOUSE
29	79	6.7	550	1	Q9J948_MOUSE
30	79	6.7	552	1	Q9J948_MOUSE
31	78.5	6.7	108	1	VGLH_HSVEL
32	78.5	6.7	108	1	KV1H_HUMAN
33	78	6.6	480	1	SAHH_XANAC

34	78	6.6	480	1	SAHH_XYLPA	O9pej1 xylella fas
35	78	6.6	485	1	SAHH_MESCR	P93253 mesembryant
36	78	6.6	3038	1	TRIO_HUMAN	O75962 homo sapien
37	77.5	6.6	226	1	C79A_HUMAN	P11912 homo sapien
38	77.5	6.6	345	1	OPCM_BOVIN	P11834 bos taurien
39	77.5	6.6	345	1	OPCM_HUMAN	O14982 homo sapien
40	77	6.6	109	1	KV01_RAT	P01681 rattus norv
41	76.5	6.5	129	1	KV3M_HUMAN	P18136 homo sapien
42	76.5	6.5	466	1	SAHH_BRUME	O8ye49 bruceella me
43	76.5	6.5	1203	1	PTC2_HUMAN	O9y6c5 homo sapien
44	76	6.5	109	1	LV2E_HUMAN	P01708 homo sapien
45	76	6.5	114	1	KV4A_HUMAN	P01625 homo sapien

ALIGNMENTS

RESULT 1

CTLA4_HUMAN STANDARD; PRT; 223 AA.
ID CTLA4_HUMAN
AC P16410; O8WKJ1; Q96P43; Q9UKN9;
DT 01-AUG-1990 (Rel. 15, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytotoxic T-lymphocyte protein 4 precursor (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD152 antigen).
GN CTLA4 OR CD152.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RX MEDLINE=21601151; PubMed=11735222;
RA Ling V., Wu P.W., Finnerty H.F., Agostino M.J., Graham J.R., Chen S., Justiff J., Fisk G.J., Miller C.P., Collins M.;
RT "Assembly and annotation of human chromosome 2q33 sequence containing the CD28, CTLA4, and ICOS gene cluster: analysis by computational, comparative, and microarray approaches.";
RL Genomics 78:155-168(2001).
[2]
RX MEDLINE=91318145; PubMed=1713603;
RA Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F., Goistein P.;
RT "CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mouse and human as to sequence, message expression, gene structure, and chromosomal location.";
RL J. Immunol. 147:1037-1044(1991).
[4]
RX MEDLINE=38-223 FROM N.A.
RA TISSUE=Lymphocytes;
RC MEDLINE=89120925; PubMed=3220103;
RA Datsvach P., Mattei M.-G., Goistein P., Lefranc M.-P.;
RT "Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of protein sequence between murine and human CTLA-4 cytoplasmic domains.";
RL Eur. J. Immunol. 18:1901-1905(1988).
[5]
RX MEDLINE=99425274; PubMed=10493833;
RA Ling V., Wu P.W., Finnerty H.F., Sharpe A.H., Gray G.S., Collins M.;
RT "Complete sequence determination of the mouse and human CTLA4 gene loci: cross-species DNA sequence similarity beyond exon borders.";
RL Genomics 60:341-355(1999).
[6]
RX MEDLINE=91341416; PubMed=1714933;
RA FUNCTION.

RA Linsley P.S., Brady W., Urnes M., Griesmaire L.S., Damlé N.K.,
 RA Ledbetter J.A.;
 RT "CTLA-4 is a second receptor for the B cell activation antigen B7.";
 RL J. Exp. Med. 174:561-569(1991).
 (7)
 RP STRUCTURE BY NMR OF 37-165.
 RX MEDLINE=97372889; PubMed=9228944;
 RA Metzler W.J., Bajorath U., Fenderson W., Shaw S.Y., Constantine K.L.,
 RA Linsley P.S.;
 RA Naemura J., Leytze G., Peach R.J., Lavoie T.B., Mueller L.,
 RT "Solution structure of human CTLA-4 and delineation of a CD80/CD86
 RT binding site conserved in CD28.";
 RL Nat. Struct. Biol. 4:527-531(1997).
 (8)
 RN VARIANT ALA-17, AND ASSOCIATION WITH IDDM12.
 RX MEDLINE=97402209; PubMed=9259273;
 RA Maron M.P., Raffel L.J., Garchon H.-J., Jacob C.O., Serrano-Rios M.,
 RA Martinez Larrad M.T., Teng W.-P., Park Y., Zhang Z.-X.,
 RA Goldstein D.R., Tao Y.-W., Beaurain G., Bach J.-F., Huang H.-S.,
 RA Luo D.-F., Zeidler A., Rotter J.I., Yang M.C.K., Modilevsky T.,
 RA MacLaren N.K., She J.-X.;
 RT "Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4
 RT polymorphisms in multiple ethnic groups.";
 RL Hum. Mol. Genet. 6:1275-1282(1997).
 (9)
 RN POLYMORPHISM, AND ASSOCIATION WITH COELIAC DISEASE.
 RX MEDLINE=9205840; PubMed=10189842;
 RA Djilali-Saiah I., Schmitz J., Harfouch-Hamoud E., Mougnot J.-F.,
 RA Bach J.-F., Gallat-Zucman S.;
 RT "CTLA-4 gene polymorphism is associated with predisposition to coeliac
 RT disease.";
 RL Gut 43:187-189(1998).
 (10)
 RN VARIANT ALA-17, AND ASSOCIATION WITH TAO.
 RX MEDLINE=99402177; PubMed=10475192;
 RA Vaidya B., Imrie H., Petros P., Dickinson J., McCarthy M.I.,
 RA Kendall-Taylor P., Pearce S.H.S.;
 RT "Cytotoxic T lymphocyte antigen-4 (CTLA-4) gene polymorphism confers
 RT susceptibility to thyroid associated orbitopathy.";
 RL Lancet 354:743-744(1999).
 (11)
 RN VARIANT ALA-17, AND ASSOCIATION WITH GRD.
 RX MEDLINE=92085252; PubMed=10924276;
 RA Chistyakov D.A., Savost' anov K.V., Turakulov R.I., Petunina N.A.,
 RA Trukhina L.V., Kudinova A.V., Balabolkin M.I., Nosikov V.V.;
 RT "Complex association analysis of Graves disease using a set of
 RT polymorphic markers.";
 RL Mol. Genet. Metab. 70:214-218(2000).
 (12)
 RN VARIANT ALA-17.
 RX MEDLINE=20395844; PubMed=10903931;
 RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,
 RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.B.,
 RA Knowles J.A.;
 RT "Familial primary pulmonary hypertension (gene PPH1) is caused by
 RT mutations in the bone morphogenetic protein receptor-II gene.";
 RL Am. J. Hum. Genet. 67:737-744(2000).
 (13)
 RN FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 (CD80) AND B7-2 (CD86).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC lymphoid tissues.
 CC -1- POLYMORPHISM: The variant Ala-17 is associated with an increased
 CC risk for autoimmune disorders as Graves disease (GRD), type I
 CC insulin-dependent diabetes mellitus (IDDM12), and thyroid-
 CC associated orbitopathy (TAO). The variant Thr-17 is associated
 CC with predisposition to coeliac disease, a gluten sensitive
 CC enteropathy characterized by small bowel mucosal atrophy.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD152 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd152.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF411058; AAL40932.1; -;
 DR EMBL; AF414120; AAL07473.1; -;
 DR EMBL; M74363; AAA52127.1; -;
 DR EMBL; M37245; AAA52773.1; -;
 DR EMBL; M37243; AAA52773.1; JOINED.
 DR EMBL; M37244; AAA52773.1; JOINED.
 DR EMBL; AF142144; AAF02499.1; -;
 DR PIR; S08614; S08614.
 DR PDB; 1AH1; 15-APR-98.
 DR PDB; 1H6E; 28-NOV-01.
 DR PDB; 1I85; 04-APR-01.
 DR PDB; 1I8L; 04-APR-01.
 DR Genew; HGNC:2505; CTLA4.
 DR MIM; 123890; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
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 KW 3d-structure; Polymorphism.
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 FT DOMAIN 36 161
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 FT CARBOHYD 113 113
 FT VARIANT 17 17
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:09 ; Search time 47.4949 Seconds
(without alignments)
745.259 Million cell updates/sec

Title: US-09-772-103-2

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1174	100.0	223	23	ABG32819 Human cytotoxic T-
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5	1170	99.7	223	23	AAU74508 Human cytotoxic T-
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7	1159	98.7	223	18	AAW25111 Soluble human CTLA
8	1159	98.7	223	22	AAU00687 Human CTLA4 protei
9	1159	98.7	223	23	ABH79934 Human CTLA4. Homo

10	1103.5	94.0	234	20	AAV41133 Human CTLA4 protei
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14	1015	86.5	223	21	AAV32280 Cat CTLA-4 recepto
15	1015	86.5	223	23	AAO17735 Peline CTLA-4. Fe
16	1015	86.5	223	23	AAU78123 Peline cytotoxic T
17	1006	85.7	223	23	AAV15122 Porcine CTLA-4 sol
18	984.5	83.9	211	20	AAW87560 Human CTLA4 recept
19	983	83.7	212	16	AAW60134 CTLA4 receptor fus
20	983	83.7	212	20	AAV43479 Pull length CTLA4
21	983	83.7	212	20	AAW81584 Human CTLA4 recept
22	983	83.7	212	23	ABW78106 Human CTLA4 recept
23	983	83.7	212	23	AAU75124 Human CTLA4 recept
24	983	83.7	212	24	ABP56715 Human CTLA4 recept
25	983	83.4	212	14	AAW31040 Human CTLA4 recept
26	979	83.4	212	23	AAU75133 Human CTLA4 recept
27	979	83.3	212	23	AAU75126 Human CTLA4 recept
28	978	83.3	212	23	AAU75132 Human CTLA4 recept
29	977	83.2	212	23	AAU75132 Human CTLA4 recept
30	977	83.2	223	22	AAU00686 Porcine CTLA4 prot
31	976	83.1	212	23	AAU75131 Human CTLA4 recept
32	972	82.8	212	23	AAU75127 Human CTLA4 recept
33	972	82.8	212	23	AAU75129 Human CTLA4 recept
34	971	82.7	212	23	AAU75130 Human CTLA4 recept
35	970	82.6	187	20	AAV41130 Human CTLA4 recept
36	970	82.6	187	20	AAW97615 Human CTLA recepto
37	970	82.6	187	20	AAW97610 Human CTLA recepto
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ALIGNMENTS

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AC AAG6519;
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XX 22-OCT-2001 (first entry)
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DR
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XX Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
KW T cell; humanized antibody; autoimmune disorder; graft rejection;
KW allergy.
XX
XX Homo sapiens.
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XX MO200154732-A1.
XX
XX 02-AUG-2001.
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XX 26-JAN-2001; 2001MO-US02653.
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XX 27-JAN-2000; 2000US-0178473.
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XX (GEMT ) GENETICS INST INC.
XX
XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
XX O'Hara D, Hinton P, Tsurushita N;
XX WPI, 2001-483195/52.
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XX N-PSDB; AAH76437.

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 673684

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	1159	98.7	223	10	US-09-988-545-21
5	1159	98.7	223	12	US-09-928-267-18
6	1159	98.7	223	12	US-09-928-267-21
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9	1152	98.1	223	14	US-10-107-828-26
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15	983	83.7	212	15	US-10-057-288-12	Sequence 12, Appl
16	983	83.7	212	15	US-10-155-514-2	Sequence 2, Appl
17	983	83.2	223	12	US-09-928-267-17	Sequence 17, Appl
18	977	83.2	223	15	US-09-928-267-22	Sequence 22, Appl
19	977	83.2	223	15	US-10-225-519-6	Sequence 6, Appl
20	977	83.2	223	15	US-09-988-545-20	Sequence 20, Appl
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22	878	74.8	223	12	US-10-077-106-5	Sequence 7, Appl
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35	661.5	56.3	383	15	US-09-865-321-8	Sequence 4, Appl
36	661.5	56.3	383	11	US-09-898-195A-19	Sequence 16, Appl
37	661.5	56.3	383	15	US-10-057-288-14	Sequence 309, App
38	661.5	56.3	383	15	US-10-155-514-16	Sequence 307, App
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; Publication No. US2003016531A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; FILE REFERENCE: P2A
; CURRENT APPLICATION NUMBER: US/10/077,106
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,757
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
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Db 181 LTAVALSKMLKKRSPLTGGVYVMPPEBCECKOPFYFIPIN 223

RESULT 3

US-10-211-207-3
; Sequence 3, Application US/10211207
; Publication No. US20030004113A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/211,207
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/077,106
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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RESULT 4

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; Patent No. US20020164697A1
; GENERAL INFORMATION:
; APPLICANT: Lehar, Sophie
; APPLICANT: Manning, Stephen
; APPLICANT: Coyte, Anthony J.
; APPLICANT: Gutierrez-Ramos, Jose-Carlos
; TITLE OF INVENTION: No. US20020164697A1e1 Th2-Specific Molecules and Uses Thereof
; FILE REFERENCE: 5800-10B
; CURRENT APPLICATION NUMBER: US/09/989,545
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/166,229
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/258,670
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
US-09-989-545-21

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Db 1 MACLGFORHKAQNLNATRTWPCCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Qy 61 ASFGKATEVRVTVLRQADSVTEVCATYMMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
Db 61 ASFGKATEVRVTVLRQADSVTEVCATYMMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
Qy 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCDPSDFLMTLAAVSSGLFFYSFL 180
Db 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCDPSDFLMTLAAVSSGLFFYSFL 180
Qy 181 LTAVALSKMLKKRSPLTGGVYVMPPEBCECKOPFYFIPIN 223
Db 181 LTAVALSKMLKKRSPLTGGVYVMPPEBCECKOPFYFIPIN 223

RESULT 5

US-09-928-267-18
; Sequence 18, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Podor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 223
; TYPE: PRT
; ORGANISM: human
US-09-928-267-18

Query Match 98.7%; Score 1159; DB 12; Length 223;
Best Local Similarity 98.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGSSGNQVNLTIQGLR 120
DB 61 ASPGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYLIGINGTQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLIGINGTQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTEPECEKOPQYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTEPECEKOPQYFIPIN 223

RESULT 6
US-09-928-267-21
; Sequence 21, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Podor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 223
; TYPE: PRT
; ORGANISM: human
US-09-928-267-21

Query Match 98.7%; Score 1159; DB 12; Length 223;
Best Local Similarity 98.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGSSGNQVNLTIQGLR 120
DB 61 ASPGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYLIGINGTQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLIGINGTQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180

QY 181 LTAVALSKMLKKRSPLTGGVYVMPTEPECEKOPQYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTEPECEKOPQYFIPIN 223

RESULT 7
US-10-225-519-8
; Sequence 8, Application US/10225519
; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Costa, Cristina
; APPLICANT: Pizzoloto, Maryellen C.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CE
; FILE REFERENCE: 33-CIP
; CURRENT APPLICATION NUMBER: US/10/225,519
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/29151
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: US 60/161,186
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-519-8

Query Match 98.7%; Score 1159; DB 15; Length 223;
Best Local Similarity 98.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGSSGNQVNLTIQGLR 120
DB 61 ASPGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYLIGINGTQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLIGINGTQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTEPECEKOPQYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTEPECEKOPQYFIPIN 223

RESULT 8
US-10-207-655-101
; Sequence 101, Application US/10207655
; Publication No. US20030118592A1

; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-101

Query Match 98.7%; Score 1159; DB 15; Length 223;
Best Local Similarity 98.7%; Pred. No. 1,2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLLFFLFIPIVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLLFFLFIPIVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
DB 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
QY 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKQOPFYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKQOPFYFIPIN 223

RESULT 9

US-10-107-828-26
; Sequence 26, Application US/10107828
; Publication No. US20020115831A1
; GENERAL INFORMATION:
; APPLICANT: Tamatani, Takuya
; APPLICANT: Tezuka, Katsunari
; TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
; FILE REFERENCE: 06501-039002
; CURRENT APPLICATION NUMBER: US/10/107, 828
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/561,308B
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/JP98/00837
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: JAPAN 09-62290
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: JAPAN 10-62217
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-828-26

Query Match 98.1%; Score 1152; DB 14; Length 223;
Best Local Similarity 98.2%; Pred. No. 6,1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLLFFLFIPIVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLLFFLFIPIVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
DB 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
QY 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKQOPFYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKQOPFYFIPIN 223

RESULT 10
US-10-107-907-26
; Sequence 26, Application US/10107907

Publication No. US20020151685A1
; GENERAL INFORMATION:
; APPLICANT: Tamatani, Takuya
; APPLICANT: Tezuka, Katsunari
; TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
; FILE REFERENCE: 06501-039002
; CURRENT APPLICATION NUMBER: US/10/107,907
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/561,308
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/JP98/00837
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: JAPAN 09-62290
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: JAPAN 10-62217
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-907-26

Query Match 98.1%; Score 1152; DB 14; Length 223;
Best Local Similarity 98.2%; Pred. No. 6,1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLLFFLFIPIVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLLFFLFIPIVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
DB 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
QY 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKQOPFYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKQOPFYFIPIN 223

RESULT 11

US-10-107-868-26
; Sequence 26, Application US/10107868
; Publication No. US20020156242A1
; GENERAL INFORMATION:
; APPLICANT: Tamatani, Takuya
; APPLICANT: Tezuka, Katsunari
; TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
; FILE REFERENCE: 06501-039002
; CURRENT APPLICATION NUMBER: US/10/107, 868
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/561,308
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 09/383,551
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: PCT/JP98/00837
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: JAPAN 09-62290
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: JAPAN 10-62217
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT

ORGANISM: Homo sapiens
US-10-107-868-26

Query Match 98.1%; Score 1152; DB 14; Length 223;
Best Local Similarity 98.2%; Pred. No. 6.1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLITIOGLR 120
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLITIOGLR 120
QY 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTEBECEKOPFYPIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTEBECEKOPFYPIPIN 223

RESULT 12

US-10-301-056-26
Sequence 26, Application US/10301056
Publication No. US20030083472A1
GENERAL INFORMATION:
APPLICANT: Tamaki, Takuya
APPLICANT: Tezuka, Katsunari
TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
FILE REFERENCE: 06501-039001
CURRENT APPLICATION NUMBER: US/10/301,056
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/383,551
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: PCT/JP98/00837
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: JAPAN 09-62290
PRIOR FILING DATE: 1997-02-27
PRIOR APPLICATION NUMBER: JAPAN 10-62217
PRIOR FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 223
TYPE: PRT
ORGANISM: Homo sapiens
US-10-301-056-26

Query Match 98.1%; Score 1152; DB 15; Length 223;
Best Local Similarity 98.2%; Pred. No. 6.1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLITIOGLR 120
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLITIOGLR 120
QY 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTEBECEKOPFYPIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTEBECEKOPFYPIPIN 223

RESULT 13

US-09-303-510-10
Sequence 10, Application US/09303510A
Patent No. US20020028208A1
GENERAL INFORMATION:
APPLICANT: Collision, Ellen W.
APPLICANT: Haeh, Stephen M.
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
FILE REFERENCE: 54954
CURRENT APPLICATION NUMBER: US/09/303,510A
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,869
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 223
TYPE: PRT
ORGANISM: Feline
US-09-303-510-10

Query Match 86.5%; Score 1015; DB 9; Length 223;
Best Local Similarity 85.7%; Pred. No. 9e-97;
Matches 191; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLITIOGLR 120
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLITIOGLR 120
QY 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTEBECEKOPFYPIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTEBECEKOPFYPIPIN 223

RESULT 14

US-09-303-040-10
Sequence 10, Application US/09303040
Patent No. US20020051792A1
GENERAL INFORMATION:
APPLICANT: Winslow, Barbara J.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,870
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 223
TYPE: PRT
ORGANISM: feline CTLA-4
US-09-303-040-10

Query Match 86.5%; Score 1015; DB 9; Length 223;
Best Local Similarity 85.7%; Pred. No. 9e-97;
Matches 191; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60


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Db      1 MACGRRRGAQDLASRTWPCIALFSLFIPVFSKGMHVAHPAVVLASSRGVASFVCEY 60
Qy      61 ASPGKATEVRVTVLROADSVTEVCATYMMGNELTFLDSTICTGSSGNQVNLITQGLR 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 GSSGNAXKFRVTVLRQTGSCMTVCATYTVENELAFINDSTCTGSSGNQVNLITQGLR 120
Qy      121 AMDTGLYICKVELMYPPIYLGINGAQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFL 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 AMDTGLYICKVELMYPPIYAGMGNGTQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFL 180
Qy      181 LTAVSLSKMLKKRSLTTGVYVMPTPECEKQFPYFIPIN 223
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 ITAVSLSKMLKKRSLTTGVYVMPTPECEKQFPYFIPIN 223
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RESULT 15

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US-09-898-195A-17
; Sequence 17, Application US/09898195A
; Publication No. US20030083246A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Robert
; APPLICANT: Carr, Suzanne
; APPLICANT: Hagerty, David
; APPLICANT: Beach, Robert J
; APPLICANT: Becker, Jean-Claude
; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
; FILE REFERENCE: D0030NP/30436.55USU1
; CURRENT APPLICATION NUMBER: US/09/898,195A
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/215,913
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-195A-17
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Query Match 83.7%; Score 983; DB 11; Length 212;

Best Local Similarity 91.9%; Pred. No. 1.7e-93;

Matches 192; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

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Qy      15 LATRTWPCITLFLFLFIPVCKAMHVAOPAVVLASSRGIASFVCEYASPKATEVRVTVL 74
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      4 LRTQRTLSLVIALLPSSASMAHVAQPAVVLASSRGIASFVCEYASPKATEVRVTVL 63
Qy      75 ROADSVTEVCATYMMGNELTFLDSTICTGSSGNQVNLITQGLRAMDGLYICKVELM 134
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      64 ROADSVTEVCATYMMGNELTFLDSTICTGSSGNQVNLITQGLRAMDGLYICKVELM 123
Qy      135 YPPPYLIGINGAQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLTTAVSLSKMLKKRS 194
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      124 YPPPYLIGINGAQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLTTAVSLSKMLKKRS 183
Qy      195 PLTTGVYVMPTPECEKQFPYFIPIN 223
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 PLTTGVYVMPTPECEKQFPYFIPIN 212
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Search completed: December 2, 2003, 06:56:44
Job time : 32.1156 secs

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:40:15 ; Search time 17.1886 Seconds
(without alignments)
548.928 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174

Sequence: 1 MACLCFORHKAQLNATRTW.....MPPTPECEKQFPYFIFIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 segs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1158	98.6	223	3	US-08-228-208A-17
2	1103.5	94.0	234	1	US-08-505-058-1
3	1103.5	94.0	234	2	US-08-459-818-21
4	1103.5	94.0	234	2	US-08-889-666-21
5	1103.5	94.0	234	2	US-08-465-078-21
6	1103.5	94.0	234	2	US-08-725-776-21
7	1103.5	94.0	234	2	US-08-488-062-21
8	1015	86.5	223	4	US-09-303-040-10
9	970	82.6	187	1	US-08-067-684-14
10	970	82.6	187	1	US-08-008-898-14
11	970	82.6	187	2	US-08-459-818-14
12	970	82.6	187	2	US-08-889-666-14
13	970	82.6	187	2	US-08-465-078-14
14	970	82.6	187	2	US-08-725-776-14
15	970	82.6	187	2	US-08-488-062-14
16	970	82.6	187	3	US-08-488-062-14
17	967	82.4	187	5	US-08-228-208A-14
18	857	73.0	223	3	PCT-US95-06726-36
19	804.5	68.5	234	1	US-08-505-058-2
20	804.5	68.5	234	2	US-08-459-818-22
21	804.5	68.5	234	2	US-08-889-666-22
22	804.5	68.5	234	2	US-08-465-078-22
23	804.5	68.5	234	2	US-08-725-776-22
24	804.5	68.5	234	2	US-08-488-062-22
25	667.5	56.9	374	4	US-09-227-595-24
26	667	56.8	374	4	US-09-227-595-26
27	667	56.8	374	4	US-09-227-595-28

28	648	55.2	124	3	US-08-630-172-4	Sequence 4, Appli
29	648	55.2	124	3	US-09-375-419-4	Sequence 4, Appli
30	648	55.2	357	3	US-08-630-172-20	Sequence 20, Appli
31	648	55.2	357	3	US-09-375-419-20	Sequence 20, Appli
32	638.5	54.4	253	2	US-08-459-818-20	Sequence 20, Appli
33	638.5	54.4	253	2	US-08-889-666-20	Sequence 20, Appli
34	638.5	54.4	253	2	US-08-465-078-20	Sequence 20, Appli
35	638.5	54.4	253	2	US-08-725-776-20	Sequence 20, Appli
36	638.5	54.4	253	2	US-08-488-062-20	Sequence 20, Appli
37	638.5	54.4	502	2	US-08-459-818-19	Sequence 19, Appli
38	638.5	54.4	502	2	US-08-889-666-19	Sequence 19, Appli
39	638.5	54.4	502	2	US-08-465-078-19	Sequence 19, Appli
40	638.5	54.4	502	2	US-08-725-776-19	Sequence 19, Appli
41	638.5	54.4	502	2	US-08-488-062-19	Sequence 19, Appli
42	606	51.6	238	4	US-09-227-595-30	Sequence 30, Appli
43	606	51.6	238	4	US-09-227-595-32	Sequence 32, Appli
44	592	50.4	137	3	US-08-804-180C-2	Sequence 2, Appli
45	563	48.0	109	4	US-09-460-384-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-08-228-208A-17
; Sequence 17, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linalley, Peter S.
; APPLICANT: Lebetter, Jeffrey A.
; APPLICANT: Brady, William K.
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: C11A4/CD28g HYBRID FUSION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-228-208A-17

Query Match 98.6%; Score 1158; DB 3; Length 223;
Best Local Similarity 98.7%; Pred. No. 5.5e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDLSICTGTSSGNQVNLTIQGLR 120
DB 61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDLSICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLPFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLPFYSFL 180
QY 181 LTAVALSKMLKKRSPILTTGVYVYMPPEBCECKQFQYFPIPIN 223
DB 181 LTAVALSKMLKKRSPILTTGVYVYMPPEBCECKQFQYFPIPIN 223

RESULT 2

US-08-505-058-1
; Sequence 1, Application US/08505058
; Patent No. 5773253
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Peach, Robert
; TITLE OF INVENTION: CT1A4 Mutant Molecules and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,058
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.30US11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-9031
; TELEFAX: 310-445-1140
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-505-058-1

Query Match 94.0%; Score 1103.5; DB 1; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60

DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDLSICTGTSSGNQVNLTIQGLR 118
DB 61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDLSICTGTSSGNQVNLTIQGLR 120
QY 119 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPC-----PDSDFLLMTLAAVSS 172
DB 121 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCXXXXXXPDSDFLLMTLAAVSS 180
QY 173 GLFFYSFLITAVSLSKMLKKRSPILTTGVYVYMPPEBCECKQFQYFPIPIN 223
DB 181 GLFFYSFLITAVSLSKMLKKRSPILTTGVYVYMPPEBCECKQFQYFPIPIN 234

RESULT 3

US-08-459-818-21
; Sequence 21, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dame, Nith K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CT1A4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeg 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-9031
; TELEFAX: 310-445-1140
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-818-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCCKAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDLSICTGTSSGNQVNLTIQGLR 118
DB 61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDLSIXICTGTSSGNQVNLTIQGLR 120
QY 119 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPC-----PDSDFLLMTLAAVSS 172
DB 121 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCXXXXXXPDSDFLLMTLAAVSS 180

Tue Dec 2 07:01:18 2003

us-09-772-103-2.rat

Page 3

QY 173 GLFFYSFLTT-AVSLSKMLKKRSPLTGGVYVMPTEPECE--KOFOPYFIPIN 223
Db 181 GLFFYSFLTTAAVSLSKMLKKRSPLTGGVYVMPTEPECEKXKOPFYFIPIN 234

RESULT 4
US-08-889-666-21
; Sequence 21, Application US/08889666
; Patent No. 5885379
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dangle, Milton K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-889-666-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLNATRTWPCITLLFLLFIPVPCAMHVAQPAVVLASSRGISAFVCEY 60
Db 1 MACLGFORHKAQNLNATRTWPCITLLFLLFIPVPCAMHVAQPAVVLASSRGISAFVCEY 60
QY 61 ASPEKATEVRVTYLRQADSOVTEVCAATYMGNELTFILDSSXICTGTSSGNQVNLITIG 118
Db 61 ASPEKATEVRVTYLRQADSOVTEVCAATYMGNELTFILDSSXICTGTSSGNQVNLITIG 120
QY 119 LRAMDGLIYICKVELMPPPYTL-GINGAQIYVIDEPC-----PDSDFLMLTAAVSS 172
Db 119 LRAMDGLIYICKVELMPPPYTL-GINGAQIYVIDEPC-----PDSDFLMLTAAVSS 172
QY 121 LRAMDGLIYICKVELMPPPYTLGIGNGTOIYVIDEPCXXXXXPSDFLMLTAAVSS 180
Db 121 LRAMDGLIYICKVELMPPPYTLGIGNGTOIYVIDEPCXXXXXPSDFLMLTAAVSS 180
QY 173 GLFFYSFLTT-AVSLSKMLKKRSPLTGGVYVMPTEPECE--KOFOPYFIPIN 223
Db 181 GLFFYSFLTTAAVSLSKMLKKRSPLTGGVYVMPTEPECEKXKOPFYFIPIN 234

RESULT 5
US-08-465-078-21
; Sequence 21, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dangle, Milton K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-078-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLNATRTWPCITLLFLLFIPVPCAMHVAQPAVVLASSRGISAFVCEY 60
Db 1 MACLGFORHKAQNLNATRTWPCITLLFLLFIPVPCAMHVAQPAVVLASSRGISAFVCEY 60
QY 61 ASPEKATEVRVTYLRQADSOVTEVCAATYMGNELTFILDSSXICTGTSSGNQVNLITIG 118
Db 61 ASPEKATEVRVTYLRQADSOVTEVCAATYMGNELTFILDSSXICTGTSSGNQVNLITIG 120
QY 119 LRAMDGLIYICKVELMPPPYTL-GINGAQIYVIDEPC-----PDSDFLMLTAAVSS 172
Db 119 LRAMDGLIYICKVELMPPPYTL-GINGAQIYVIDEPC-----PDSDFLMLTAAVSS 172
QY 121 LRAMDGLIYICKVELMPPPYTLGIGNGTOIYVIDEPCXXXXXPSDFLMLTAAVSS 180
Db 121 LRAMDGLIYICKVELMPPPYTLGIGNGTOIYVIDEPCXXXXXPSDFLMLTAAVSS 180
QY 173 GLFFYSFLTT-AVSLSKMLKKRSPLTGGVYVMPTEPECE--KOFOPYFIPIN 223
Db 181 GLFFYSFLTTAAVSLSKMLKKRSPLTGGVYVMPTEPECEKXKOPFYFIPIN 234
RESULT 6
US-08-725-776-21
; Sequence 21, Application US/08725776

```
Patent No. 5968510
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienier, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-21

Query Match          94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSS--ICTGTSSGNOVNLTIQ 118
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSSXXICTGTSSGNOVNLTIQ 120
QY 119 LRAMDGLYICVKEVLMYPPYYL-GINGAQIYVIDPPEC-----PDSDFLLMTILAAVSS 172
DB 121 LRAMDGLYICVKEVLMYPPYYLXGINGQIYVIDPPECXXXXXKPSDFLLMTILAAVSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKNPTEBECE--KQOPYFPIPIN 223
DB 181 GLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKNPTEBECEXXKQOPYFPIPIN 234

RESULT 7
US-08-488-062-21
Sequence 21, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
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APPLICANT: Brady, William
APPLICANT: Kienier, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
CLASSIFICATION: 435
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-062-21

Query Match          94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSS--ICTGTSSGNOVNLTIQ 118
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSSXXICTGTSSGNOVNLTIQ 120
QY 119 LRAMDGLYICVKEVLMYPPYYL-GINGAQIYVIDPPEC-----PDSDFLLMTILAAVSS 172
DB 121 LRAMDGLYICVKEVLMYPPYYLXGINGQIYVIDPPECXXXXXKPSDFLLMTILAAVSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKNPTEBECE--KQOPYFPIPIN 223
DB 181 GLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKNPTEBECEXXKQOPYFPIPIN 234

RESULT 8
US-09-303-040-10
Sequence 10, Application US/09303040
Patent No. 655671
GENERAL INFORMATION:
APPLICANT: Winslow, Barbara J.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
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EARLIER APPLICATION NUMBER: 60/083,870
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 223
TYPE: PRT
ORGANISM: feline CTLA-4
US-09-103-040-10

Query Match 86.5%; Score 1015; DB 4; Length 223;
Best Local Similarity 85.7%; Pred. No. 2.6e-96;
Matches 191; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MACLGROHRAQANTLRTMPCULLPFLFIPPCAMHVAQAVVLASSRGIAFVCEY 60
DB 1 MACFGRHRAQADLARSRTMPCULPFLFIPFSCAMHVAQAVVLASSRGIAFVCEY 60
QY 61 ASPKATEVRVTVLRQADSOVTEVCAATYMGNELTFELDSICTGSSGNVLTIOGR 120
DB 61 GSSGNNAKFRVTVLRQDSGMTVCATYVENELAFINDSTCTGSSGNVLTIOGR 120
QY 121 AMDTGLYICKVELMPPPYLLGNGAQIYVIDPBCPDSPFLMILAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLLGNGAQIYVIDPBCPDSPFLMILAAVSSGLFFYSFL 180
QY 181 LRAVSLSKMLKRSPLTGYVYVMPTPECEKOPPIPIPN 223
DB 181 ITAVSLSKMLKRSPLTGYVYVMPTPECEKOPPIPIPN 223

RESULT 9

US-08-067-684-14
Sequence 14, Application US/08067684
Patent No. 5434131
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nalin K.
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheldon & Mak
STREET: 225 South Lake Avenue, Suite 900
CITY: Pasadena
STATE: California
COUNTRY: U.S.A.
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/067,684
FILING DATE: 26-MAY-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 7848-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310/312-9900
TELEFAX: 310/479-8340
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-067-684-14

Query Match 82.6%; Score 970; DB 1; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNELT 96
DB 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNELT 96
QY 97 FLDDSICTGSSGNVLTIOGLRAMDTGLYICKVELMPPPYLLGNGAQIYVIDPBP 156
DB 61 FLDDSICTGSSGNVLTIOGLRAMDTGLYICKVELMPPPYLLGNGAQIYVIDPBP 120
QY 157 CPDSDFLMILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYVMPTPECEKOPQ 216
DB 121 CPDSDFLMILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYVMPTPECEKOPQ 180
QY 217 PYPIPIPN 223
DB 181 PYPIPIPN 187

RESULT 10

US-08-008-898-14
Sequence 14, Application US/08008898
Patent No. 5770197
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nalin K.
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheldon & Mak
STREET: 201 South Lake Avenue, Suite 800
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,898
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/723,617
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 7848
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-008-898-14
Query Match 82.6%; Score 970; DB 1; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNELT 96

Db 1 AMHVAQPAVVLAASRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60
Qy 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPIYLLGIGNGAQIYVIDPBP 156
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPIYLLGIGNGAQIYVIDPBP 120
Qy 157 CPDSDFLMLTAAVSSGLFFYSFLTLTAVALSKMLKKRSPLTGGVYVVMPTPEBCEKQFO 216
Db 121 CPDSDFLMLTAAVSSGLFFYSFLTLTAVALSKMLKKRSPLTGGVYVVMPTPEBCEKQFO 180
Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 11
US-08-459-818-14
Sequence 14, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Milton K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fastseq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459, 818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 37 AMHVAQPAVVLAASRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96
Db 1 AMHVAQPAVVLAASRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60
Qy 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPIYLLGIGNGAQIYVIDPBP 156
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPIYLLGIGNGAQIYVIDPBP 120
Qy 157 CPDSDFLMLTAAVSSGLFFYSFLTLTAVALSKMLKKRSPLTGGVYVVMPTPEBCEKQFO 216
Db 121 CPDSDFLMLTAAVSSGLFFYSFLTLTAVALSKMLKKRSPLTGGVYVVMPTPEBCEKQFO 180

Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 12
US-08-889-666-14
Sequence 14, Application US/08889666
Patent No. 5885379
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Milton K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889, 666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 37 AMHVAQPAVVLAASRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96
Db 1 AMHVAQPAVVLAASRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60
Qy 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPIYLLGIGNGAQIYVIDPBP 156
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPIYLLGIGNGAQIYVIDPBP 120
Qy 157 CPDSDFLMLTAAVSSGLFFYSFLTLTAVALSKMLKKRSPLTGGVYVVMPTPEBCEKQFO 216
Db 121 CPDSDFLMLTAAVSSGLFFYSFLTLTAVALSKMLKKRSPLTGGVYVVMPTPEBCEKQFO 180
Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 13
US-08-465-078-14
Sequence 14, Application US/08465078
Patent No. 5685796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 96
DB 1 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 60
QY 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 156
DB 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 120
QY 157 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 216
DB 121 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 180
QY 217 PYFIPIN 223
DB 181 PYFIPIN 187

RESULT 14
US-08-725-776-14
Sequence 14, Application US/08725776
Patent No. 5968510
GENERAL INFORMATION:

APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 96
DB 1 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 60
QY 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 156
DB 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 120
QY 157 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 216
DB 121 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 180
QY 217 PYFIPIN 223
DB 181 PYFIPIN 187

RESULT 15
US-08-488-062-14
Sequence 14, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-062-14

Query Match 82.6%; Score 970; DB 2; length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIAFPVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNEELT 96
DB 1 AMHVAQPAVVLASSRGIAFPVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNEELT 60
QY 97 FLDDSICTGTSSGNQVLLTIGLRAMDYGLYICKVELMYPFPYLLGIGNGAQIYVIDPEP 156
DB 61 FLDDSICTGTSSGNQVLLTIGLRAMDYGLYICKVELMYPFPYLLGIGNGAQIYVIDPEP 120
QY 157 CPDSDFLMLTILAAVSSGLFFYSFLTAVSLSKMLKKRSPLTGTVYVMPTPECEKQFQ 216
DB 121 CPDSDFLMLTILAAVSSGLFFYSFLTAVSLSKMLKKRSPLTGTVYVMPTPECEKQFQ 180
QY 217 PYPIPIN 223
DB 181 PYPIPIN 187

Search completed: December 2, 2003, 06:46:00
Job time: 18.1886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:39:15 ; Search time 9.08722 Seconds

(without alignments)
1354.605 Million cell updates/sec

Title: US-09-772-103-8

Perfect score: 655

Sequence: 1 MDPVOQIFSLISASVILS.....COQMSYPLTFGGTKVEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	502	76.6	130	2	A32513
2	499	76.2	130	1	JL0079
3	498	76.0	235	2	S25058
4	491	75.0	140	2	PL0013
5	478	73.0	130	2	S04573
6	466	71.1	130	2	B32456
7	463.5	70.8	107	2	S36264
8	463.5	70.8	107	2	S36264
9	463.5	70.8	108	2	B49047
10	455.5	69.5	129	2	S40349
11	454.5	69.4	107	2	S52793
12	454.5	69.4	129	2	S40317
13	454.5	69.4	129	2	S52789
14	452.5	69.1	123	2	S40331
15	452.5	69.1	125	2	S40331
16	451.5	68.9	108	2	S19674
17	451.5	68.9	132	2	S40334
18	447.5	68.3	125	2	S40316
19	446	68.1	129	1	KWMS78
20	445.5	68.0	127	1	S40367
21	444.5	67.9	108	1	KIHURV
22	444.5	67.9	108	1	S36277
23	441.5	67.4	108	1	KIHUNN
24	441.5	67.4	117	2	S46371
25	441.5	67.4	125	2	S40350
26	441.5	67.3	132	2	S05268
27	439.5	67.1	129	2	S40369
28	437.5	66.8	108	2	S36279
29	436.5	66.6	108	1	KIHUNE

30	436	66.6	106	2	PC2397	anti-tetanus toxin
31	435.5	66.5	107	2	I69017	anti-HIV1 envelope
32	435.5	66.5	108	1	KIHUNU	Ig kappa chain V-I
33	435.5	66.5	125	2	S40353	Ig kappa chain V-J
34	434.5	66.3	110	2	S44118	Ig kappa chain V-J
35	434.5	66.3	117	2	S46376	Ig kappa chain V-J
36	434.5	66.3	123	2	S40313	Ig kappa chain V-J
37	432.5	66.0	108	1	KIHUNU	Ig kappa chain V-I
38	431	65.8	109	1	KIHUNV	Ig kappa chain V-I
39	430.5	65.7	109	2	S31998	Ig kappa chain - h
40	430.5	65.7	129	1	KIHUND	Ig kappa chain pre
41	430	65.6	124	2	S40336	Ig kappa chain V-J
42	429.5	65.6	108	2	S44122	Ig kappa chain V-I
43	429.5	65.6	131	2	S40352	Ig kappa chain V-J
44	429.5	65.6	139	2	S40365	Ig kappa chain - h
45	429.5	65.6	141	2	A49134	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

A32513

Ig kappa chain precursor V region (MRU22) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C/Accession: A32513

R/Kofler, R.; Strohal, R.; Balderae, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A>Title: Immunoglobulin kappa light chain variable region gene complex organization and

A/Reference number: A94689; MUID:88331394; PMID:3138286

A/Accession: A32513

A/Molecule type: DNA

A/Residues: 1-130 <KOF>

A/Cross-references: GB:M20834; NID:g196943; PID:AAA38846.1; PID:g196944

C/Keywords: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterocleamer; immunoglobulin

F38-113/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 502; DB 2; Length 130;

Best Local Similarity 74.6%; Pred. No. 2.7e-33;

Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

Qy	1	MDPVOQIFSLISASVILSRGDIOMTQSPSLASVGDVITCSATSI--TYMSYQ	58
Db	1	MDPVOQIFSLISASVILSRGQIVLTQSPALMSFGERVTTCSSSVSSITLYIQ	60
Qy	59	OKPKAKRLIYDTNSLASGVPSRFGSGGCTDYTLTISLQPDFAITYYCOQMSYPLT	118
Db	61	OKPSSPKLMTYTSNLSAGVPAFPSSGSGCTSYSLTSSMEADDAITYYCOQSGPFT	120
Qy	119	FGGCTKVEIK 128	
Db	121	FGGCTKLEIK 130	

RESULT 2

JL0079

Ig kappa chain precursor V region (anti-phenylloxazalone 6f6) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999

C/Accession: JL0079; A49044; B49044

R/Karltun, M.; Rocca-Serra, J.; Maekela, O.

Mol. Immunol. 25, 859-865, 1988

A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re-

A/Reference number: JL0076; MUID:89096973; PMID:3211160

A/Accession: JL0079

A/Molecule type: mRNA

A/Residues: 1-130 <KAA>

A/Cross-references: GB:M27792; NID:g197159

A/Experimental source: mRNA clones for anti-phenylloxazalone antibody 6f6

A/Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10

A/Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation

R.Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Bernandez, A.; Gherardi, E.
 Eur. J. Immunol. 22, 1627-1634, 1992
 A>Title: Non-random features of the repertoire expressed by the members of one V kappa g
 A:Reference number: A49044; MUID:92289826; PMID:1601044
 A:Accession: A49044
 A:Molecule type: DNA
 A:Residues: 1-25 <MTL>
 A:Cross-references: GB:S37663; NID:9250214; PIDN:AA822331.1; PID:9250217
 A>Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBI:106809)
 A:Accession: B49044
 A:Molecule type: DNA
 A:Residues: 114-116 <MTL>
 A:Cross-references: GB:S37664; NID:9250215; PIDN:AA822332.1; PID:9250218
 A:Experimental source: BALB/c germ-line
 A>Note: sequences extracted from NCBI backbone: partial nucleotide sequences of 13 addit
 A>Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:106822)
 C:Genetics:
 A:Gene: V(Kappa)Ox1
 A:Introns: 17/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap
 hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:45-109/Diulfide bonds: #status predicted

Query Match 76.2%; Score 499; DB 1; Length 130;
 Best Local Similarity 74.2%; Pred. No. 4.7e-33;
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPVOVIFSLISASVILSRGDIOMTOSPSLSASVGDRTVITCSATSTYMSWYQOK 60
 Db 1 MDPVOVIFSLISASVILSRGDIOMTOSPSLSASVGDRTVITCSATSTYMSWYQOK 60

Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
 Db 61 SGTSPKRWIYDTSKLSAGVPSRFGSGSGTSLTSSMEADATYTCQOMSSYPLTFG 120

Qy 121 GGTVEIK 128
 Db 121 AGTKLEK 128

RESULT 3
 S25058
 Ig kappa chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S25058
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
 Submitted to the EMBL Data Library, July 1992
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neopop specific n
 A:Reference number: S25057
 A:Accession: S25058
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-235 <PIS>
 A:Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 498; DB 2; Length 235;
 Best Local Similarity 74.2%; Pred. No. 9.9e-33;
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPVOVIFSLISASVILSRGDIOMTOSPSLSASVGDRTVITCSATSTYMSWYQOK 60
 Db 1 MDPVOVIFSLISASVILSRGDIOMTOSPSLSASVGDRTVITCSATSTYMSWYQOK 60

Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
 Db 61 SGTSPKRWIYDTSKLSAGVPSRFGSGSGTSLTSSMEADATYTCQOMSSYPLTFG 120

Db 61 SGTSPKRWIYDTSKLSAGVPSRFGSGSGTSLTSSMEADATYTCQOMSSYPLTFG 120
 Qy 121 GGTVEIK 128
 Db 121 AGTKLEK 128

RESULT 4
 PLO013
 Ig kappa chain precursor V region (4C11) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: PLO013
 R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988
 A>Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: PLO011; MUID:86142853; PMID:3125424
 A:Accession: PLO013
 A:Molecule type: mRNA
 A:Residues: 1-140 <CHB>
 A:Experimental source: Cell line 4C11
 C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:46-55/Region: complementarity-determining 1
 F:71-77/Region: complementarity-determining 2
 F:110-118/Region: complementarity-determining 3
 F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 75.0%; Score 491; DB 2; Length 140;
 Best Local Similarity 74.2%; Pred. No. 2.2e-33;
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPVOVIFSLISASVILSRGDIOMTOSPSLSASVGDRTVITCSATSTYMSWYQOK 60
 Db 1 MDPVOVIFSLISASVILSRGDIOMTOSPSLSASVGDRTVITCSATSTYMSWYQOK 60

Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
 Db 61 PDIAPKLMYDTSNLSAGVPSRFGSGSGTSLTSSMEADATYTCQOMSSYPLTFG 120

Qy 121 GGTVEIK 128
 Db 121 GGTLEMK 128

RESULT 5
 S04573
 Ig kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
 C:Accession: S04573
 R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balders, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
 Eur. J. Immunol. 17, 91-95, 1987
 A>Title: Molecular analysis of the murine lupus-associated anti-self response: involvem
 A:Reference number: S04573; MUID:87133856; PMID:3102255
 A:Accession: S04573
 A:Molecule type: mRNA
 A:Residues: 1-130 <KOF>
 A:Cross-references: EMBL:X14620; NID:925031; PIDN:CAA32773.1; PID:925032
 A>Note: the authors translated the codon AGC for residue 47 as Asn
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 478; DB 2; Length 130;
 Best Local Similarity 70.8%; Pred. No. 2.2e-31;
 Matches 92; Conservative 22; Mismatches 14; Indels 2; Gaps 1;

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:49 ; Search time 5.9716 Seconds

(without alignment)
1008.007 Million cell updates/sec

Title: US-09-772-103-8

Perfect score: 655

Sequence: 1 MDPQVQIFSFLLISAVLIS.....COQMSYPLTFGGGTRKVEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446	68.1	129	KV4A_MOUSE	P01680 mus musculu
2	444.5	67.9	108	KV1P_HUMAN	P01608 homo sapien
3	441.5	67.4	108	KV1V_HUMAN	P04330 homo sapien
4	436.5	66.6	108	KV1O_HUMAN	P01607 homo sapien
5	435.5	66.5	108	KV1B_HUMAN	P01594 homo sapien
6	434.5	66.3	108	KV1J_HUMAN	P80362 homo sapien
7	433.5	66.0	108	KV1H_HUMAN	P01600 homo sapien
8	431	65.8	109	KV1T_HUMAN	P01612 homo sapien
9	430.5	65.7	129	KV1X_HUMAN	P04332 homo sapien
10	427.5	65.3	108	KV1S_HUMAN	P01611 homo sapien
11	427.5	65.3	129	KV1W_HUMAN	P04431 homo sapien
12	422.5	64.5	108	KV1F_HUMAN	P01598 homo sapien
13	422.5	64.5	108	KV1M_HUMAN	P01605 homo sapien
14	421.5	64.4	108	KV1G_HUMAN	P01599 homo sapien
15	421.5	64.4	108	KV1R_HUMAN	P01610 homo sapien
16	420.5	64.2	108	KV1L_HUMAN	P01593 homo sapien
17	418.5	63.9	108	KV1A_HUMAN	P01604 homo sapien
18	416	63.5	107	KV1D_HUMAN	P01596 homo sapien
19	413.5	63.1	108	KV1K_HUMAN	P01603 homo sapien
20	412.5	63.0	108	KV1E_HUMAN	P01597 homo sapien
21	412.5	63.0	108	KV1N_HUMAN	P01606 homo sapien
22	412	62.9	108	KV1C_MOUSE	P04945 mus musculu
23	409.5	62.5	108	KV1Q_HUMAN	P01609 homo sapien
24	408.5	62.4	108	KV1I_HUMAN	P01595 mus musculu
25	408.5	62.4	108	KV1J_MOUSE	P01643 mus musculu
26	408.5	62.4	117	KV1J_HUMAN	P01602 homo sapien
27	401.5	61.3	117	KV1I_HUMAN	P01601 homo sapien
28	399	60.9	107	KV1F_MOUSE	P04940 mus musculu
29	398.5	60.8	112	KV1U_HUMAN	P01613 mus musculu
30	394	60.2	107	KV1I_MOUSE	P04943 mus musculu
31	393	60.0	107	KV1G_MOUSE	P04941 mus musculu
32	393	60.0	107	KV1H_MOUSE	P04942 mus musculu
33	392	59.8	107	KV6J_MOUSE	P04944 mus musculu

34	389	59.4	133	1	KV4B_HUMAN	P06313 homo sapien
35	388.5	59.3	108	1	KV5K_MOUSE	P01644 mus musculu
36	388.5	59.3	134	1	KV4C_HUMAN	P06314 homo sapien
37	386.5	59.0	136	1	KV5B_MOUSE	P01648 mus musculu
38	385.5	58.9	108	1	KV5O_MOUSE	P01648 mus musculu
39	384	58.6	129	1	KV3L_HUMAN	P01635 homo sapien
40	383.5	58.5	108	1	KV5L_MOUSE	P01645 mus musculu
41	383.5	58.5	108	1	KV5M_MOUSE	P01646 mus musculu
42	383.5	58.5	108	1	KV5N_MOUSE	P01647 mus musculu
43	383.5	58.5	149	1	KV5A_MOUSE	P01633 mus musculu
44	381	58.2	129	1	KV3M_HUMAN	P01636 homo sapien
45	379	57.9	107	1	KV6A_MOUSE	P01675 mus musculu

ALIGNMENTS

RESULT 1
KV4A_MOUSE STANDARD; PRT; 129 AA.

AC P01680;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max B.R., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107. ";
RL Cell 26:57-66(1981).
CC -I- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; J00577; AAA8780.1; -;
DR EMBL; V00780; CA24157.1; -;
DR PIR; A01943; KWS7B.
DR HSSP; P01679; 2PB3.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22
FT CHAIN 1 129 IG KAPPA CHAIN V-IV REGION S107B.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 58 72 FRAMEWORK-2.
FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 80 111 FRAMEWORK-3.
FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 128 FRAMEWORK-4.
FT DISULFID 45 111 BY SIMILARITY.
FT NON TER 129
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072D6F6B4 CRC64;

Query Match 68.1%; Score 446; DB 1; Length 129;

Best Local Similarity 66.9%; Pred. No. 3.5e-36;
Matches 87; Conservative 21; Mismatches 18; Indels 4; Gaps 2;

QY 1 MFOVQIFSELLISAVISRGDICTQSPSSLSASVGRVITTCATSSI--TMSWQ 58
DB 1 MLQVQIIXFLPILVISTVSKRGNVLTQSPALMAASLGQKVTMTCSASSSVSYLHWQ 60
QY 59 QKPGKAPKLLIYDTSNMGASVPSFSGSGGTDYTLTISLQPEDPATYTCQOMSSYP 118
DB 61 QKSGASPKRLIHTSLASGVAPRPSGSGSGTSTLITISVLAEDDATYTCQOMSGYP-- 118
QY 119 FCGGTKEIK 128
DB 119 FCGGTKEIK 128

RESULT 2

KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hillechmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
RT Hope-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hillechmann N., Barnikol H.U., Hesse M., Langer B., Ponstingl H.,
RA Stejmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCR-JONES PROTEIN.
CC PIR; A91638; KIHURY.
DR HSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003006; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11762 MW; F5ACED5A313DF3A CRC64;

Query Match 67.9%; Score 444.5; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 4e-36;
Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 81

DB 1 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 60

QY 82 RPSGSGGTDYTLTISLQPEDPATYTCQOMSSYP 128
DB 61 RPSGSGGTDYTLTISLQPEDPATYTCQOMSSYP 107

RESULT 3

KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwyer F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RT Mol. Immunol. 23:73-78(1986).
RN [2]
RP PIR; A01878; KIHUBN.
DR HSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 67.4%; Score 441.5; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 7.7e-36;
Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 81
DB 1 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 60

QY 82 RPSGSGGTDYTLTISLQPEDPATYTCQOMSSYP 128
DB 61 RPSGSGGTDYTLTISLQPEDPATYTCQOMSSYP 107

RESULT 4

KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DS Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:33:29 ; Search time 21.8093 Seconds

(without alignments)
1514.523 Million cells updates/sec

Title: US-09-772-103-8

Perfect score: 655
Sequence: 1 MDPVOQIRSFLLISASVILS.....CQMSRYPLTRGGKRVK 128

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_Archea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacterioid:*
17: SP_Archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	510	77.9	134	11	Q8VDD0	Q8VDD0 mus musculu
2	477	72.8	235	11	Q91W12	Q91W12 mus musculu
3	448	68.4	107	4	Q96SA9	Q96SA9 homo sapien
4	436.5	66.6	108	4	Q9UL77	Q9UL77 homo sapien
5	428.5	65.4	108	4	Q9UL70	Q9UL70 homo sapien
6	417	63.7	107	4	Q9UL81	Q9UL81 homo sapien
7	415	63.4	112	11	Q8K1F3	Q8K1F3 mus musculu
8	413	63.1	112	11	Q8K1F2	Q8K1F2 mus musculu
9	411	62.7	106	5	Q9U410	Q9U410 schistosoma
10	410.5	62.7	108	4	Q9UL79	Q9UL79 homo sapien
11	405.5	61.9	234	11	Q8R062	Q8R062 mus musculu
12	403.5	61.6	233	11	Q91WS9	Q91WS9 mus musculu
13	397	60.6	112	11	Q8K1F0	Q8K1F0 mus musculu
14	397	60.6	114	11	Q8K1F1	Q8K1F1 mus musculu
15	396.5	60.5	116	4	Q96PF6	Q96PF6 homo sapien
16	395.5	60.4	109	11	Q920E6	Q920E6 mus musculu

17	387.5	59.2	234	11	Q8VCP0	Q8VCP0 mus musculu
18	387.5	59.2	298	11	Q9QIF0	Q9QIF0 mus musculu
19	387	59.1	109	4	Q9UL78	Q9UL78 homo sapien
20	386.5	59.0	107	11	Q9JL84	Q9JL84 mus musculu
21	379.5	57.9	214	11	Q9JL85	Q9JL85 mus musculu
22	375.5	57.3	234	11	Q9JL78	Q9JL78 mus musculu
23	375	57.3	109	4	Q9UL85	Q9UL85 homo sapien
24	372.5	56.9	97	11	Q9JL76	Q9JL76 mus musculu
25	370.5	56.6	234	4	Q8NEK1	Q8NEK1 homo sapien
26	369.5	56.4	108	11	Q8VJ30	Q8VJ30 mus musculu
27	364.5	55.6	108	4	Q9UL83	Q9UL83 homo sapien
28	363.5	55.5	111	11	Q920E9	Q920E9 mus musculu
29	361.5	55.2	101	11	Q9JL78	Q9JL78 mus musculu
30	361	55.1	109	4	Q9UL86	Q9UL86 homo sapien
31	357.5	54.6	127	11	Q925S9	Q925S9 mus musculu
32	341	52.1	238	11	Q9PM37	Q9PM37 mus musculu
33	337	51.5	238	11	Q8VCI6	Q8VCI6 mus musculu
34	337	51.5	239	11	Q8VCS5	Q8VCS5 mus musculu
35	328	50.1	239	4	Q8NEK0	Q8NEK0 mus musculu
36	328.5	49.8	107	11	Q9ER29	Q9ER29 mus musculu
37	324	49.5	239	4	Q8TCD0	Q8TCD0 homo sapien
38	324	49.5	241	11	Q921A6	Q921A6 mus musculu
39	321.5	49.1	99	11	Q9JL74	Q9JL74 mus musculu
40	319.5	48.8	103	11	Q9JL80	Q9JL80 mus musculu
41	319.5	48.8	239	11	Q8K0F8	Q8K0F8 mus musculu
42	310.5	47.4	234	11	Q8R028	Q8R028 mus musculu
43	309	47.2	104	11	Q9JL82	Q9JL82 mus musculu
44	297.5	45.4	114	4	Q9UL80	Q9UL80 homo sapien
45	294.5	45.0	109	6	Q9N0W5	Q9N0W5 oryctolagus

ALIGNMENTS

RESULT 1

Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembl P.;
RT "Targeting T cells to the CNS."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ16311; CAC94866.1; -
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MW; CFPD8E2236B2DOCF CRC64;
Query Match 77.9%; Score 510; DB 11; Length 134;
Best Local Similarity 77.3%; Pred. No. 4.9e-44;
Matches 99; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
QY 1 MDPVOQIRSFLLISASVILSRGDIQMTQSPSSLSASVGRVITTCATSSITYSWYQOK 60

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Db 1 MDPQVQIFSLISASVILSRQIVLTQSPALMSAPGKVTMTCSASSISYMHMYQK 60
Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGDTYTLTISLQPEDFATYYCOQMSYPLTFG 120
Db 61 POTSFKRWIYDTSKLSAGVPARFSGSGSTSLTISNMEADATYYCHQNSIFPWTG 120
Qy 121 GGTKEIK 128
Db 121 GGTKEIK 128

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RESULT 2

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Q91W12 PRELIMINARY; PRT; 235 AA.

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AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Unknown (Protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AA006643.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD586FEF CRC64;

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Query Match 72.8%; Score 477; DB 11; Length 235;
Best Local Similarity 71.1%; Pred. No. 2,2e-40;
Matches 91; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

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Qy 1 MDPQVQIFSLISASVILSRQIVLTQSPALMSAPGKVTMTCSASSISYMHMYQK 60
Db 1 MDPQVQIFSLISASVILSRQIVLTQSPALMSAPGKVTMTCSASSISYMHMYQK 60
Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGDTYTLTISLQPEDFATYYCOQMSYPLTFG 120
Db 61 POTSFKRWIYDTSKLSAGVPARFSGSGSTSLTISNMEADATYYCHQNSIFPWTG 120
Qy 121 GGTKEIK 128
Db 121 GGTKEIK 128

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RESULT 3

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Q96SA9 PRELIMINARY; PRT; 107 AA.

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AC 096SA9.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;

```

```

RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AB68785.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

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Query Match 68.4%; Score 448; DB 4; Length 107;
Best Local Similarity 85.0%; Pred. No. 7.2e-38;
Matches 91; Conservative 6; Mismatches 8; Indels 2; Gaps 2;

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Qy 23 DIQMTGSPSSLSASVGVDRVITTCASATSI-TYMSWYQKPGKAPKLLIYDTSNLSAGVPS 81
Db 1 DIQMTGSPSSLSASVGVDRVITTCASATSI-TYMSWYQKPGKAPKLLIYDTSNLSAGVPS 60
Qy 82 RFGSGSGDTYTLTISLQPEDFATYYCOQMSYPLTFGSGTKEIK 128
Db 61 RFGSGSGDTYTLTISLQPEDFATYYCOQ-SYSTLTFGSGTKEIK 106

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RESULT 4

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Q9UL77 PRELIMINARY; PRT; 108 AA.

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AC 09UL77.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;

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Query Match 66.6%; Score 436.5; DB 4; Length 108;
Best Local Similarity 82.2%; Pred. No. 1.1e-36;
Matches 88; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

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Qy 23 DIQMTGSPSSLSASVGVDRVITTCASATSI-TYMSWYQKPGKAPKLLIYDTSNLSAGVPS 81
Db 1 DIQMTGSPSSLSASVGVDRVITTCASATSI-TYMSWYQKPGKAPKLLIYDTSNLSAGVPS 60
Qy 82 RFGSGSGDTYTLTISLQPEDFATYYCOQMSYPLTFGSGTKEIK 128
Db 61 RFGSGSGDTYTLTISLQPEDFATYYCOQ-SYSTSWTFGSGTKEIK 107

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:09 : Search time 27.2617 Seconds
(without alignments) 745.259 Million cell updates/sec

Title: US-09-772-103-8
Sequence: 1 MDPQVGFSLISASVILS.....CQMSYPLFGGTVEIK 128
Perfect score: 655

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	100.0	128	22	AA66522
2	609	93.0	128	17	AA90684
3	600	91.6	128	21	AA77597
4	600	91.6	128	22	AA77597
5	599	91.5	235	18	AAW41398
6	593	90.5	235	18	AAW41398
7	590	90.1	133	15	AA53345
8	590	90.1	133	20	AA78394
9	590	90.1	133	20	AA78371

10	587	89.6	126	21	AA77599	Anti-human VEGF re
11	587	89.6	126	22	AA77599	Anti-human VEGF re
12	584	89.2	130	19	AAW73179	Fragment of gangli
13	584	89.2	130	19	AAW73180	Fragment of gangli
14	584	89.2	130	20	AAW73175	Fragment of gangli
15	584	89.2	130	20	AAW73176	Fragment of gangli
16	583	89.0	235	18	AAW41410	Human chimeric ant
17	580	88.5	130	20	AAW73181	Human chimeric ant
18	580	88.5	130	20	AAW73181	Human chimeric ant
19	573	87.5	126	21	AAW77601	Human chimeric ant
20	573	87.5	126	22	AAW77601	Human chimeric ant
21	572	87.3	130	19	AAW73182	Anti-human Flt-1 a
22	572	87.3	130	20	AAW73182	Anti-human Flt-1 a
23	571	87.2	130	19	AAW73185	Human chimeric ant
24	571	87.2	130	20	AAW73185	Human chimeric ant
25	568	86.7	130	19	AAW73184	Human chimeric ant
26	568	86.7	130	20	AAW73184	Human chimeric ant
27	567	86.6	130	19	AAW73173	Human chimeric ant
28	567	86.6	130	20	AAW73173	Human chimeric ant
29	566	86.4	130	21	AAW73182	Human chimeric ant
30	564	86.1	130	19	AAW73176	Human chimeric ant
31	562	85.8	130	19	AAW73183	Human chimeric ant
32	562	85.8	130	20	AAW73179	Human chimeric ant
33	560	85.5	130	19	AAW73174	Human chimeric ant
34	560	85.5	130	20	AAW73174	Human chimeric ant
35	543	82.9	235	17	AAW66180	Human chimeric ant
36	528	80.6	128	22	AAW66521	Human chimeric ant
37	523	79.8	235	18	AAW41392	Human chimeric ant
38	520	79.4	126	21	AAW77598	Human chimeric ant
39	520	79.4	126	22	AAW77598	Human chimeric ant
40	520	79.4	128	13	AAW27050	Anti-human VEGF re
41	519	79.2	128	22	AAW69655	Anti-human VEGF re
42	518	79.1	126	19	AAW36164	Human chimeric ant
43	517	78.9	128	12	AAW13227	Human chimeric ant
44	516	78.8	129	17	AAW88108	Human chimeric ant
45	514	78.5	128	17	AAW90690	Human chimeric ant

ALIGNMENTS

RESULT 1	AA66522	AA66522 standard; Protein; 128 AA.
ID	AA66522	
AC	AA66522	
DT	22-OCT-2001	(first entry)
DE	Humanised anti-CTLA4 light chain.	
XX	Human: CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;	
XX	immunopressive; immunomodulator; antiallergic; vaccine; antibody;	
XX	T cell; humanised antibody; autoimmune disorder; graft rejection;	
XX	allergy; light chain.	
XX	Human sapiens.	
XX	Mus musculus.	
XX	Synthetic.	
XX	WO200154732-A1.	
XX	02-AUG-2001.	
XX	26-JAN-2001; 2001WO-US02653.	
XX	27-JAN-2000; 2000US-0178473.	
XX	(GENY) GENETICS INST INC.	
XX	Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;	
XX	O'Hara D, Hinton P, Tsurushita N;	
XX		

1:21 2003

us-09-772-103-8.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:44:30 ; Search time 18.4341 Seconds
(without alignments)
1280.712 Million cell updates/sec

Title: US-09-772-103-8

Sequence: 1 MDPVOQIFSLISASVILS.....CQWSSYPLTFGGCTKVEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgnt2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgnt2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgnt2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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9: /cgnt2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgnt2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgnt2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgnt2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	91.6	128	15	US-10-160-232-92
2	599	91.5	235	15	US-09-910-059-52
3	593	90.5	235	10	US-09-910-059-99
4	587	89.6	126	15	US-10-160-232-94
5	583	89.0	235	10	US-09-910-059-97
6	573	87.5	126	15	US-10-160-232-96
7	567	86.6	130	15	US-10-195-752-111
8	564	86.1	130	15	US-10-195-752-113
9	563	79.8	235	10	US-09-910-059-17
10	520	79.4	126	15	US-10-160-232-93
11	514	78.5	233	15	US-10-071-485-69
12	500	76.3	110	9	US-09-753-436-96
13	500	76.3	110	12	US-10-163-942-96
14	499	76.2	107	10	US-09-910-059-50
15	496.5	75.8	258	15	US-10-207-655-343

16	496.5	75.8	492	15	US-10-207-655-344	Sequence 344, App
17	496.5	75.8	543	15	US-10-207-655-345	Sequence 345, App
18	496.5	75.8	543	15	US-10-207-655-346	Sequence 346, App
19	496	75.7	107	10	US-09-910-059-61	Sequence 61, App1
20	495	75.6	128	12	US-10-244-821-92	Sequence 92, App1
21	493	75.3	107	10	US-09-910-059-71	Sequence 71, App1
22	493	75.3	128	15	US-10-160-232-87	Sequence 87, App1
23	490	74.8	126	15	US-10-160-232-89	Sequence 89, App1
24	490	74.8	128	11	US-09-967-719C-4	Sequence 4, App11
25	490	74.8	128	11	US-09-967-719C-6	Sequence 6, App11
26	488	74.5	235	11	US-09-795-515-5	Sequence 5, App11
27	487	74.4	106	9	US-09-796-848A-3	Sequence 3, App11
28	487	74.4	106	10	US-09-771-415-1	Sequence 1, App11
29	487	74.4	107	15	US-10-267-286A-8	Sequence 8, App11
30	487	74.4	131	15	US-10-207-655-256	Sequence 256, App
31	487	74.4	213	10	US-09-996-288-231	Sequence 231, App
32	487	74.4	213	11	US-09-996-285-231	Sequence 231, App
33	487	74.4	266	15	US-10-207-655-260	Sequence 260, App
34	487	74.4	550	15	US-10-207-655-270	Sequence 270, App
35	485	74.0	106	10	US-09-771-415-17	Sequence 17, App1
36	485	74.0	106	12	US-10-127-850-165	Sequence 165, App
37	484	73.9	106	11	US-09-996-285-54	Sequence 54, App1
38	484	73.9	106	11	US-09-996-285-54	Sequence 54, App1
39	484	73.9	106	12	US-10-020-354-54	Sequence 54, App1
40	484	73.9	213	10	US-09-996-288-211	Sequence 211, App
41	484	73.9	213	11	US-09-996-285-211	Sequence 211, App
42	483	73.7	107	10	US-09-910-059-65	Sequence 65, App1
43	482	73.6	213	9	US-09-881-823-6	Sequence 6, App11
44	482	73.6	213	10	US-09-996-288-255	Sequence 255, App
45	482	73.6	213	11	US-09-996-285-255	Sequence 255, App

ALIGNMENTS

RESULT 1
US-10-160-232-92
Sequence 92, Application US/10160232
Publication No. US2003008075A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: ITO, MIKITO
APPLICANT: HANAI, NOBORO
APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/10/160,232
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-92
Query Match 91.6%, Score 600, DB 15, Length 128,
Best Local Similarity 91.4%, Pred. No. 4e-44,
Matches 117, Conservative 5, Mismatches 6, Indels 0, Gaps 0;
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Qy 121 GGTKEVEIK 128
Db 121 GGTKEVEIK 128
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RESULT 2

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US-09-910-059-52
; Sequence 52, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic Use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: complete humanised light chain sequence
US-09-910-059-52
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Query Match 91.5%; Score 599; DB 10; Length 235;
Best Local Similarity 91.4%; Pred. No. 9, 3e-44;
Matches 117; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVGDGVITTCSSASSSVTHMYQOK 60
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Db 61 PGKAPKLLIYDTSNLASGVSPRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Qy 121 GGTKEVEIK 128
Db 121 GGTKEVEIK 128
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RESULT 3

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US-09-910-059-99
; Sequence 99, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic Use in an Adept System
; FILE REFERENCE: 1991-209
; APPLICATION NUMBER: US/09/910,059
; DATE: 2001-07-23
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; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain Fd sequence
US-09-910-059-99
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Query Match 90.5%; Score 593; DB 10; Length 235;
Best Local Similarity 90.6%; Pred. No. 3e-43;
Matches 116; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVGDGVITTCSSASSSVTHMYQOK 60
Db 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVGDGVITTCSSASSSVTHMYQOK 60
Qy 61 PGKAPKLLIYDTSNLASGVSPRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Db 61 PGKAPKLLIYDTSNLASGVSPRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Qy 121 GGTKEVEIK 128
Db 121 GGTKEVEIK 128
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RESULT 4

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US-10-160-232-94
; Sequence 94, Application US/10160232
; Publication No. US20030088075A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/10/160,232
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-94
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Query Match 89.6%; Score 587; DB 15; Length 126;
Best Local Similarity 90.6%; Pred. No. 5.1e-43;
Matches 116; Conservative 5; Mismatches 5; Indels 2; Gaps 1;
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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: December 2, 2003, 06:40:15 ; Search time 9.86613 Seconds
(without alignments)
548,928 Million cell updates/sec

Title: US-09-772-103-8

Sequence: 1 MDPQVGFSLISAVLS.....COGSSYPLTGGTKVLEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	93.0	128	3	US-08-619-491-6
2	609	93.0	128	3	PCT-US95-07302-6
3	599	91.5	235	3	US-09-171-945-52
4	593	90.1	235	3	US-09-171-945-99
5	590	90.1	133	2	US-08-116-778E-37
6	590	90.1	133	2	US-08-438-562-37
7	590	90.1	133	2	US-08-483-528B-101
8	583	89.0	235	3	US-09-171-945-97
9	567	86.6	130	4	US-09-393-385B-111
10	564	86.1	130	4	US-09-393-385B-113
11	543	82.9	235	4	US-09-011-769A-27
12	520	79.4	128	1	US-07-946-421-26
13	519	79.2	128	1	US-07-634-278-31
14	519	79.2	128	1	US-08-477-728-31
15	519	79.2	128	1	US-08-474-040-31
16	519	79.2	128	1	US-08-487-200-31
17	519	79.2	128	1	US-08-484-537-31
18	518	79.1	126	2	US-08-656-586-6
19	518	79.1	126	2	US-09-171-945-17
20	516	78.8	129	5	PCT-US95-07312-12
21	514	78.5	128	3	US-08-619-491-2
22	514	78.5	128	3	PCT-US95-07302-2
23	514	78.5	233	4	US-09-485-737B-69
24	508	77.6	106	1	US-07-634-278-35
25	508	77.6	106	1	US-07-634-278-59
26	508	77.6	106	1	US-08-477-728-35
27	508	77.6	106	1	US-08-477-728-59

28	508	77.6	106	1	US-08-474-040-35	Sequence 35, Appl
29	508	77.6	106	1	US-08-474-040-59	Sequence 59, Appl
30	508	77.6	106	1	US-08-487-200-35	Sequence 35, Appl
31	508	77.6	106	1	US-08-487-200-59	Sequence 59, Appl
32	508	77.6	106	3	US-08-484-537-35	Sequence 35, Appl
33	508	77.6	106	3	US-08-484-537-59	Sequence 59, Appl
34	506	77.3	129	2	US-08-116-778E-2	Sequence 2, Appl
35	506	77.3	129	2	US-08-438-562-2	Sequence 2, Appl
36	506	77.3	129	2	US-08-483-528B-92	Sequence 92, Appl
37	503	76.8	106	3	US-08-397-411-8	Sequence 8, Appl
38	503	76.8	213	3	US-08-397-411-12	Sequence 12, Appl
39	500	76.3	110	1	US-08-482-882-96	Sequence 96, Appl
40	500	76.3	110	2	US-08-483-389-96	Sequence 96, Appl
41	500	76.3	110	2	US-08-487-113D-96	Sequence 96, Appl
42	500	76.3	110	2	US-08-473-503-96	Sequence 96, Appl
43	500	76.3	110	2	US-08-483-932-96	Sequence 96, Appl
44	500	76.3	110	2	US-08-720-420A-96	Sequence 96, Appl
45	500	76.3	110	3	US-08-714-017-96	Sequence 96, Appl

ALIGNMENTS

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RESULT 1
US-08-619-491-6
; Sequence 6, Application US/08619491
; Patent No. 6210670
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,491
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/07302
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,963
; FILING DATE: 14-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 011823-005810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-619-491-6
; Query Match 93.0%; Score 609; DB 3; Length 128;
; Best Local Similarity 93.0%; Pred. No. 5.1e-46;
; Matches 119; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 1 MDPVOVIFSLIASVILSRGDIOMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
DB 1 MDPVOVIFSLIASVILSRGDIOMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
QY 61 PKAKPLIYDTSNLSAGVPSRFSGSGGTDTTLTISLQPEDPATYTCQOMSSYPLTFG 120
DB 61 PKAKPLIYDTSNLSAGVPSRFSGSGGTDTTLTISLQPEDPATYTCQOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 2

PCT-US95-07302-6
Sequence 6, Application PC/TUS9507302
GENERAL INFORMATION:
APPLICANT: Berg, Ellen L.
TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
TITLE OF INVENTION: Specific for E-selectin and P-selectin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: PCT/US95/07302
APPLICATION NUMBER: PCT/US95/07302
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/259,963
FILING DATE: 14-JUNE-94
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-005810PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07302-6

Query Match 93.0%; Score 609; DB 5; Length 128;
Best Local Similarity 93.0%; Pred. No. 5, 1e-48;
Matches 119; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPVOVIFSLIASVILSRGDIOMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
DB 1 MDPVOVIFSLIASVILSRGDIOMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
QY 61 PKAKPLIYDTSNLSAGVPSRFSGSGGTDTTLTISLQPEDPATYTCQOMSSYPLTFG 120
DB 61 PKAKPLIYDTSNLSAGVPSRFSGSGGTDTTLTISLQPEDPATYTCQOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 3

US-09-171-945-52
Sequence 52, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-52

Query Match 91.5%; Score 599; DB 3; Length 235;
Best Local Similarity 91.4%; Pred. No. 8, 1e-47;
Matches 117; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPVOVIFSLIASVILSRGDIOMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
DB 1 MDPVOVIFSLIASVILSRGDIOMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
QY 61 PKAKPLIYDTSNLSAGVPSRFSGSGGTDTTLTISLQPEDPATYTCQOMSSYPLTFG 120
DB 61 PKAKPLIYDTSNLSAGVPSRFSGSGGTDTTLTISLQPEDPATYTCQOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 4

US-09-171-945-99
Sequence 99, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 99
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-99

Query Match 90.5%; Score 593; DB 3; Length 235;
Best Local Similarity 90.6%; Pred. No. 2.8e-46;
Matches 116; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDPVOVIFSPFLISASVILSRGDIQMTQSPSSLSASVGRVITTCASITTSITMSWYQOK 60
DB 1 MDPVOVIFSPFLISASVILSRGDIQMTQSPSSLSASVGRVITTCASITTSITMSWYQOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISLSQPEDFATYYCOQWSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISLSQPEDFATYYCOQWSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 5

US-08-116-778E-37
Sequence 37, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIIISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYTE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-116-778E-37

Query Match 90.1%; Score 590; DB 2; Length 133;
Best Local Similarity 89.8%; Pred. No. 2.8e-46;
Matches 115; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDPVOVIFSPFLISASVILSRGDIQMTQSPSSLSASVGRVITTCASITTSITMSWYQOK 60
DB 1 MDPVOVIFSPFLISASVILSRGDIQMTQSPSSLSASVGRVITTCASITTSITMSWYQOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISLSQPEDFATYYCOQWSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISLSQPEDFATYYCOQWSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 6

US-08-438-562-37
Sequence 37, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIIISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYTE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-562-37

Query Match 90.1%; Score 590; DB 2; Length 133;
Best Local Similarity 89.8%; Pred. No. 2.8e-46;
Matches 115; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDPVOVIFSPFLISASVILSRGDIQMTQSPSSLSASVGRVITTCASITTSITMSWYQOK 60
DB 1 MDPVOVIFSPFLISASVILSRGDIQMTQSPSSLSASVGRVITTCASITTSITMSWYQOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISLSQPEDFATYYCOQWSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTISLSQPEDFATYYCOQWSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 7
US-08-483-528B-101

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; Sequence 101, Application US/084835288
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIOHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-528B-101

Query Match      90.1%; Score 590; DB 2; Length 133;
Best Local Similarity 89.8%; Pred. No. 2.8e-46;
Matches 115; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDFOVOIFSFLLISASVILSRGDIQMTQSPSSISASVGDRTVITCSATSSITTMWYQOK 60
DB 1 MHFOVOIFSFLLISASVILSRGDIQMTQSPSSISASVGDRTVITCSATSSITTMWYQOK 60
QY 61 PGKAPKLLIYDTSNLSASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQQRSSYPYTFG 120
DB 61 PGKAPKLLIYDTSNLSASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQQRSSYPYTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 8
US-09-171-945-97
; Sequence 97, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
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; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-97

Query Match      89.0%; Score 583; DB 3; Length 235;
Best Local Similarity 89.1%; Pred. No. 2.2e-45;
Matches 114; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDFOVOIFSFLLISASVILSRGDIQMTQSPSSISASVGDRTVITCSATSSITTMWYQOK 60
DB 1 MHFOVOIFSFLLISASVILSRGDIQMTQSPSSISASVGDRTVITCSATSSITTMWYQOK 60
QY 61 PGKAPKLLIYDTSNLSASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQQRSSYPYTFG 120
DB 61 PGKAPKLLIYDTSNLSASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQQRSSYPYTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 9
US-09-393-385B-111
; Sequence 111, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIOHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-393-385B-111

Query Match      86.6%; Score 567; DB 4; Length 130;
Best Local Similarity 86.7%; Pred. No. 3.2e-44;
Matches 111; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
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Tue Dec 2 07:01:20 2003

us-09-772-103-8.ra1

Page 5

Qy	1	MDFOVOVFFSFLLLISASVILSRGDIOMTOSPSLSASVGDRLVITCSAASSITMYSWYQOK	60
Db	1	MHFOVOVFFSFLLLISASVILSRGDIOMTOSPSLSASVGDRLVITCSAASSVYMHMFQOK	60
Qy	61	PGKAPKLLIYDITSNLASGVPSRPSGSGSTDTLTLSILOPEDATYCCQOMSSYPLTFG	120
Db	61	PGKAPKLLIYDITSNLASGVPSRPSGSGSTDTLTLSILOPEDATYCCQOMSSYPLTFG	120
Qy	121	GGTKVEIK	128
Db	121	GGTKVEIK	128

```

RESULT 10
US-09-393-385B-113
Sequence 113, Application US/09393385B
Patent No. 6423511
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIIISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
Zip: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4100
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-393-385B-113

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Query Match	86.1%	Score 564;	DB 4;	Length 130;
Best Local Similarity	85.9%	Pred. NO. 5.9e-44;		
Matches 110; Conservative	8;	Mismatches 10;	Indels 0;	Gaps 0

QY	1	MDFOVIFSELLISASVILSRDIDQMTPSPSLASVADRITTCASATSTITWMSYQOK	60
Db	1	MHFQVQIFSEFLLISASVILSRDIDQITPSPSLASPEDRVTITCSASSSVYWHWFQK	60
QY	61	PGKAPRLIYDTSNLASGVSRFSGSGSDTYLTLSLQPEDPATYCCQMSSEPLTFG	120
Db	61	PGAAPRLMIYTSNLSASGVPAFSGSGSTYSLTLSLQPEDPATYCCQMSSEPYTFG	120
QY			
QY	121	GGTKVEIK	128
Db	121	GGTKVEIK	128

RESULT 11
US-09-011-769A-27

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Sequence 27. Application US/09011769A
Patent No. 6436691

GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
            BLAKLEY, David C.
            DAVIES, David H.
            HENNAM, John P.
            HENNEQUIN, Laurent F.A.
            MARSHAM, Peter R.
            POWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSER: Pillsbury Madison & Sutoero, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011.769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:

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Query Match	82.9%	Score 543;	DB 4;	Length 235;
Best Local Similarity	82.8%	Pred. No. 9.1e-42;		
Matches 106;	Conservative 7;	Mismatches 15;	Indels 0;	Gaps 0

Qy 1 MPFOVQIFSEFLILSLASVILSGDILQMTQSPSLSASVGDRLTITCSATPSLITYSMTQOK 60

Db 1 MPFOVQIFSEFLILSLASVILSGDILQMTQSPSLSASVGDRLTITCSATPSLITYSMTQOK 60

Qy 61 PGKAPLTLIDYDLSNLASGVPSRFSGSGSGTYTLTISLAPEDPATYCCQOMSSYPLTFG 120

Db 61 PGKAPLTLIDYDLSNLASGVPSRFSGSGSGTYTLTISLAPEDPATYCCQOMSSYPLTFG 120

Qy 121 GGTKVEIK 128

Db 121 GGTKVEIK 128

RESULT 12
 US-07-946-421-26
 ; Sequence 26, Application US/07946421
 ; Patent No. 5558864
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Kettleborough, Catherine A.
 ; APPLICANT: Saldanha, Jose
 ; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
 ; TITLE OF INVENTION: Antibodies

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: 06-NOV-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-07-946-421-26

Query Match 79.4%; Score 520; DB 1; Length 128;
Best Local Similarity 77.3%; Pred No. 5.4e-40;
Matches 99; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVDGRVTITCSATSSITVMSWYQK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVDGRVTITCSATSSITVMSWYQK 60
QY 61 PGKAPKLLIYDTSNLASGVPRFSGSGSDTDTLTITSSLOPEDPATYTCOOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPRFSGSGSDTDTLTITSSLOPEDPATYTCOOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 13
US-07-634-278-31
Sequence 31, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-31

Query Match 79.2%; Score 519; DB 1; Length 128;
Best Local Similarity 75.0%; Pred No. 6.7e-40;
Matches 96; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVDGRVTITCSATSSITVMSWYQK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVDGRVTITCSATSSITVMSWYQK 60
QY 61 PGKAPKLLIYDTSNLASGVPRFSGSGSDTDTLTITSSLOPEDPATYTCOOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPRFSGSGSDTDTLTITSSLOPEDPATYTCOOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 14
US-08-477-728-31
Sequence 31, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-31

Query Match 79.2%; Score 519; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 6.7e-40;
Matches 96; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
DB 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFSGSGTDTYLTITSLQPEDFATYYCOOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFSGSGTDTYLTITSLQPEDFATYYCOOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 AGTKLELK 128

RESULT 15
US-08-474-040-31
Sequence 31, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-31

Query Match 79.2%; Score 519; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 6.7e-40;
Matches 96; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
DB 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFSGSGTDTYLTITSLQPEDFATYYCOOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFSGSGTDTYLTITSLQPEDFATYYCOOMSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 AGTKLELK 128

Search completed: December 2, 2003, 06:46:01
Job time: 10.8661 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:39:15; Search time 10.0811 Seconds

(Without alignments)
1354.605 Million cell updates/sec

Title: US-09-772-103-10

Perfect score: 742

Sequence: 1 MAVLVPLCLVAFPPSCVLTSQ.....MKRGYANDYWGQGTIVTVSS 142

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR.76:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	79.3	141	2	S52446
2	561.5	75.7	139	2	A32456
3	558	75.2	140	2	S55028
4	528.5	71.2	135	2	S31913
5	525	70.8	117	2	S10111
6	510	68.7	140	2	S14238
7	506	68.2	144	1	G2MS14
8	504.5	68.0	140	2	S11244
9	491	66.2	140	2	I37782
10	483.5	65.2	137	2	S31676
11	481.5	64.9	130	2	PI0087
12	478	64.4	116	2	A33932
13	478	64.4	155	2	S31511
14	476	64.2	147	2	S13519
15	475	64.0	116	1	G1MS10
16	475	63.2	112	2	S31512
17	467.5	63.0	145	2	S78055
18	467.5	63.0	130	2	S31590
19	466	62.8	114	2	S11106
20	466	62.5	115	1	HVMS14
21	464	62.5	116	2	S11102
22	464	62.5	116	2	B31807
23	464	62.5	146	2	S09711
24	459	61.9	146	2	PO0266
25	458	61.7	117	2	S38563
26	456.5	61.5	146	2	S09710
27	456	61.5	146	2	S09710

30	454	61.2	139	2	S31596	Ig heavy chain V r
31	453	61.1	140	2	A49045	Ig heavy chain V r
32	450.5	60.7	116	2	S42484	Ig heavy chain V r
33	449	60.5	114	2	S11099	Ig heavy chain V r
34	449	60.5	115	2	S11103	Ig heavy chain V r
35	447	60.2	106	2	S26322	Ig heavy chain V r
36	447	60.2	112	2	S11108	Ig heavy chain V r
37	446	60.1	135	2	S78051	Ig heavy chain V r
38	444.5	59.9	118	2	S32786	Ig heavy chain pre
39	444	59.8	121	2	S33131	Ig heavy chain (an
40	442.5	59.6	140	2	S78052	Ig heavy chain V r
41	441	59.4	114	2	S26321	Ig heavy chain pre
42	441	59.4	140	2	S54239	Ig mu heavy chain
43	441	59.4	124	2	S54244	Ig mu heavy chain
44	439	59.2	121	2	D30560	Ig heavy chain V r
45	438.5	59.1	141	2	S54236	Ig mu heavy chain

ALIGNMENTS

RESULT 1

S52446
Ig heavy chain V region precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999

C/Accession: S52446

R/Berdoz, J.; Kraehenbuhl, J.P.

Submitted to the EMBL Data Library, November 1994

A/Description: Specific amplification by the polymerase chain reaction of rearranged gen

A/Reference number: S52445

A/Accession: S52446

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-141 <BER>

A/Cross-references: EMBL:X82692; NID:g673441; PID:CAA58013.1; PID:g673442

C/Genetics: 16/1

A/Intons: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 588.5; DB 2; Length 141;

Best Local Similarity 81.0%; Pred. No. 9.5e-45;

Matches 115; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY	1	MAVLVPLCLVAFPPSCVLTSQ.....MKRGYANDYWGQGTIVTVSS 142	
DB	1	MAVLVPLCLVAFPPSCVLTSQ.....MKRGYANDYWGQGTIVTVSS 141	
QY	61	GKLEWLVGVWAGTNNYSALMSRLTISKDNKSVLSTADTAVVYCARGPH 120	
DB	61	GKLEWLVGVWAGTNNYSALMSRLTISKDNKSVLSTADTAVVYCARGPH 119	
QY	121	AMKRGYANDYWGQGTIVTVSS 142	
DB	120	STMDTPYANDYWGQGTIVTVSS 141	
RESULT 2			
A32456			
Ig heavy chain precursor V region - mouse			
C/Species: Mus musculus (house mouse)			
C/Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999			
C/Accession: A32456			
R/Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.			
J. Biol. Chem. 264, 4513-4522, 1989			
A/Title: Variable region primary structures of a high affinity anti-fluorescein immunogl			
A/Reference number: A32456; PMID:89174706; PMID:2494173			
A/Accession: A32456			
A/Status: preliminary			
A/Molecule type: mRNA			
A/Residues: 1-139 <DOM>			

A:Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317
A:Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 561.5; DB 2; Length 139;
Best Local Similarity 76.4%; Pred. No. 2.2e-42;
Matches 110; Conservative 14; Mismatches 13; Indels 7; Gaps 2;

QY 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
DB 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 120
DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 116

QY 121 AMMKR--GIAMDYWGQGTLLTVSS 142
DB 117 RLRIIFYAMDYWGQGTSLTVSS 139

RESULT 3

IS5028
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C/Accession: S55028
R:Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff, J. Mol. Biol. 248, 344-360, 1995
A>Title: Structure and specificity of the anti-digoxin antibody 40-50.
A:Reference number: S55027; MUID:95257394; PMID:7739045
A:Accession: S55028
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <JEF>

A:Cross-references: EMBL:L11403; NID:9476717; PIDN:AAA83191.1; PID:9476718
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 558; DB 2; Length 140;
Best Local Similarity 76.1%; Pred. No. 4.5e-42;
Matches 108; Conservative 15; Mismatches 17; Indels 2; Gaps 1;

QY 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
DB 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 120
DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 118

QY 121 AMMKRGVAMDYWGQGTLLTVSS 142
DB 119 PASVYDYAVDYWGQGTSLTVSS 140

RESULT 4

S31913
Ig gamma-2A chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
C/Accession: S31913
R:Bespalov, I.A.; Hlyanov, P.A.; Lukashovich, L.V.; Lunev, V.B.; Tribush, S.S.; Gaponova
submitted to the EMBL Data Library, January 1993
A:Reference number: S31913
A:Accession: S31913
A:Molecule type: mRNA
A:Residues: 1-115 <BRS>
A:Cross-references: EMBL:X70822; NID:957921; PIDN:CAA50153.1; PID:957922
A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-11/Domain: signal sequence #status predicted <SIG>
F:12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 528.5; DB 2; Length 135;
Best Local Similarity 70.4%; Pred. No. 1.7e-39;
Matches 100; Conservative 19; Mismatches 16; Indels 7; Gaps 1;

QY 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
DB 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 120
DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 116

QY 121 AMMKRGVAMDYWGQGTLLTVSS 142
DB 117 ELVYFDYWGQGTLLTVSS 135

RESULT 5

S10111
Ig heavy chain V region (clone 26) precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S10111
R:Kaartinen, M.; Solin, M.L.; Maekela, O. EMBO J. 8, 1743-1748, 1989
A>Title: 'Allelic' forms of immunoglobulin V genes in different strains of mice.
A:Reference number: S10111; MUID:89356648; PMID:2767052
A:Accession: S10111
A:Molecule type: mRNA
A:Residues: 1-117 <KAA>

A:Cross-references: EMBL:X15471; NID:950005; PIDN:CAA33499.1; PID:950006
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 525; DB 2; Length 117;
Best Local Similarity 85.3%; Pred. No. 2.9e-39;
Matches 99; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
DB 1 MAVLVFLCLVAFPCSVLSQVQLQESGPGLVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 116
DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAIVYCAR 116

RESULT 6

S14238
Ig gamma-1 chain precursor (15C5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S14238
R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D. Eur. J. Biochem. 192, 767-775, 1990
A>Title: Construction and characterization of a recombinant murine monoclonal antibody d.
A:Reference number: S14236; MUID:91006173; PMID:2209622
A:Accession: S14238
A:Molecule type: mRNA
A:Residues: 1-140 <VAN>
A:Cross-references: EMBL:X56392; NID:951619; PIDN:CAA39803.1; PID:9747853
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:26-108/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 510; DB 2; Length 140;

1	506	68.2	144	1	HV43_MOUSE	P01819 mus musculi
2	475	64.0	116	1	HV45_MOUSE	P01821 mus musculi
3	464	62.5	115	1	HV44_MOUSE	P01820 mus musculi
4	415	55.9	135	1	HV02_XENLA	P20957 xenopus laevis
5	414.5	55.9	146	1	HV21_HUMAN	P06331 homo sapiens
6	390.5	52.6	137	1	HV46_MOUSE	P01822 mus musculi
7	379	51.1	117	1	HV26_HUMAN	P01825 homo sapiens
8	376	50.7	129	1	HV2F_HUMAN	P01824 homo sapiens
9	366	49.3	136	1	HV01_XENLA	P20964 homo sapiens
10	361	48.7	116	1	HV61_MOUSE	P20956 xenopus laevis
11	352	46.2	116	1	HV60_MOUSE	P18532 mus musculi
12	342.5	47.4	147	1	HV2H_HUMAN	P18531 mus musculi
13	341.5	46.0	120	1	HV2B_HUMAN	P04438 homo sapiens
14	339	45.7	121	1	HV3J_HUMAN	P01815 homo sapiens
15	332.5	44.8	126	1	HV3K_HUMAN	P01771 homo sapiens
16	332	44.7	113	1	HV47_MOUSE	P01722 homo sapiens
17	329.5	44.4	122	1	HV3G_HUMAN	P01823 mus musculi
18	325	43.8	119	1	HV2C_HUMAN	P01768 homo sapiens
19	324	43.7	119	1	HV2D_HUMAN	P01816 homo sapiens
20	323.5	43.7	136	1	HV2C_RABIT	P01817 homo sapiens
21	321.5	43.6	117	1	HV2E_MOUSE	P01829 oryctolagus
22	321.5	42.3	136	1	HV16_MOUSE	P18533 mus musculi
23	316.5	42.7	122	1	HV3H_HUMAN	P01783 mus musculi
24	310	41.8	121	1	HV2E_HUMAN	P01769 homo sapiens
25	309	41.6	140	1	HV02_MOUSE	P01818 homo sapiens
26	308.5	41.6	114	1	HV2A_RABIT	P01746 mus musculi
27	307.5	41.4	119	1	HV40_MOUSE	P01827 oryctolagus
28	306	41.2	117	1	HV2B_RABIT	P01840 mus musculi
29	305	41.1	115	1	HV3D_HUMAN	P01828 oryctolagus
30	305	41.1	142	1	HV01_RAT	P01765 homo sapiens
31	304.5	41.0	114	1	HV3B_HUMAN	P01763 homo sapiens
32	304.5	41.0	119	1	HV3F_MOUSE	P01807 mus musculi
33	304.5	41.0	126	1	HV2A_HUMAN	P01814 homo sapiens

45	292	39.4	120	1	HV03_MOUSE	pol1747	mus musculi
44	292.5	39.6	119	1	HV1A_RAB1T	pol1826	homo sapiens
43	293.5	39.6	119	1	HV48_MOUSE	pol1777	homo sapiens
42	294	39.8	138	1	HV48_MOUSE	pol1980	homo sapiens
41	295.5	39.8	116	1	HV37_HUMAN	pol1767	homo sapiens
40	296	39.9	115	1	HV3F_HUMAN	pol1812	mus musculi
39	297	40.0	117	1	HV42_MOUSE	pol1773	homo sapiens
38	299	40.3	119	1	HV3L_HUMAN	pol1770	homo sapiens
37	302	40.7	119	1	HV3I_HUMAN	pol1981	catarrhini a
36	302	40.7	116	1	HV05_CARAU	pol1751	mus musculi
35	302.5	40.8	139	1	HV07_MOUSE	pol1755	mus musculi
34	304.5	41.0	137	1	HV11_MOUSE	pol1755	mus musculi

ID	HYV3 MOUSE	STANDARD;	PRT;	144 AA.
AC	P01819;			
AD	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	IG heavy chain V region MOPC 141 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81012133; PubMed=6774256;			
RA	Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;			
RT	"Two types of somatic recombination are necessary for the generation			
RT	of complete immunoglobulin heavy-chain genes.";			
RL	Nature 286:676-683(1980).			
CC	-1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A			
CC	DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES ICG2B.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			

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DR	EMBL; V00768; CAA24149.1; -.
DR	PIR; A02094; GZMS14.
DR	HSSP; P01825; 7FAB.
DR	InterPro; IPR007110; IG_1like.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PR00047; ig_1.
DR	SMART; SM00406; IgY; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
KW	Immunoglobulin v region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT	DOMAIN 20 130 IG-LIKE.
FT	NON_TER 144 144
SEQUENCE	144 AA; 15759 MW; 8E47A7CB3706D3DA CRC64;

Query Match	68.2%	Score 506;	DB 1;	Length 144;
-------------	-------	------------	-------	-------------

Matches 97; Conservative 15; Mismatches 30; Indels 2; Gaps 1;

QY 1 MAVLVLFCLVAFPSCVLSOVQIQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWRQP 60

Db 1 MAVIALFLCLATFPSCILSQVQLKESGPGLVAPSQSLITCTVSGFSLTGYGVNWRQP 60

QY 61 GKGLEMLGVIWAGTTNYSALMSRLTISKDTSKNQVSLKSSVTADTAVYCCARGP-- 118

Db 61 GKGLEMLGWTGNSSTYNSLTNRLLTKTKNSKSVFLKNNLSLOTDDTARYCASVSIV 120
 QY 119 PHAMKRGYADYWGGLTYVSS 142
 Db 121 YGGRSDKFTLIDTWGOSTVTVSS 144

RESULT 2

HV45_MOUSE
 ID HV45_MOUSE STANDARD; PRT; 116 AA.

AC P01821;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT Ig heavy chain V region MC101 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

MDLINE=82075900; PubMed=6273429;

Kataoka T., Nikaido T., Miyata T., Moriaki K., Honjo T.;

"The nucleotide sequences of rearranged and germline immunoglobulin

RT VH genes of a mouse myeloma MC101 and evolution of VH genes in

mouse."

RL J. Biol. Chem. 257:277-285 (1982).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC or send an email to license@isb-sib.ch).

CC EMBL; J00502; AAA38515.1; -

DR PIR; A02096; GIMSI0.

DR HSSP; P01772; 2PB4.

DR InterPro; IPR007110; IG_1like.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IG_1.

DR SMART; SM00406; IGV_1.

DR SMART; PS50835; IG_1like.

DR PROSITE; PS50835; IG_1like.

DR Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 116 IG HEAVY CHAIN V REGION MC101.

FT DOMAIN 20 >116 IG-LIKE.

FT NON_TER 116 116

FT SEQUENCE 116 AA; 12593 MW; 8079A6EB7C552B3B CRC64;

QY

Query Match

Best Local Similarity 75.0%; Score 475; DB 1; Length 116;

Matches 87; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 116

DT 15-SBP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region P014 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=81012133; PubMed=6774258;

RA Sakano H., Maki R., Kuroawa Y., Roeder W., Tonegawa S.;

RT "Two types of somatic recombination are necessary for the generation

RT of complete immunoglobulin heavy-chain genes."

RT Nature 286:676-683 (1980).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; V00767; CAA24148.1; -

DR PIR; A02095; HVMS14.

DR PDB; 1A7N; 29-APR-98.

DR PDB; 1A7O; 29-APR-98.

DR PDB; 1A7P; 29-APR-98.

DR PDB; 1A7R; 29-APR-98.

DR PDB; 1G7H; 17-JAN-01.

DR PDB; 1G7I; 17-JAN-01.

DR PDB; 1G7J; 17-JAN-01.

DR PDB; 1G7M; 17-JAN-01.

DR PDB; 43C9; 24-JUL-02.

DR PDB; 43CA; 24-JUL-02.

DR InterPro; IPR007110; IG_1like.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IGV_V.

DR Pfam; PF00047; IGV_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_1like.

DR Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 19

FT CHAIN 20 115 IG HEAVY CHAIN V REGION P014.

FT DOMAIN 20 >115 IG-LIKE.

FT NON_TER 115 115

FT SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

QY

Query Match

Best Local Similarity 75.7%; Score 464; DB 1; Length 115;

Matches 87; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYWRPP 60

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

Db 61 GKGLEMLGVTWAGTNTYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCA 115

QY 121 AMMKRGVAMDYWGGLVTVSS 142
 DB 121 E-----GAMDYWGGLVTVSS 137

RESULT 2

Q96EYO PRELIMINARY; PRT; 613 AA.

AC Q96EYO; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=B-cell;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC011857; AAH11857.1; -

DR InterPro: IPR007110; I9_1like.

DR InterPro: IPR003006; I9_MHC.

DR Pfam: PF00047; I9_5.

DR SMART: SM00406; IGV_1.

DR PROSITE: PS00835; I9_LIKE; 5.

DR PROSITE: PS00290; I9_MHC; 3.

KW Hypothetical protein.

SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 63.0%; Score 467.5; DB 4; Length 613;

Best Local Similarity 68.3%; Pred. No. 6.9e-41;

Matches 99; Conservative 11; Mismatches 26; Indels 9; Gaps 2;

QY 1 MAVLVFLCLVAFPSCVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRP 60

DB 1 MKHLWFLVLVAAPRWVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRP 60

QY 61 GKLEWLVIMAGTNNYNSALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP-- 118

DB 61 GKLEWLVIMAGTNNYNSALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP-- 120

QY 119 -PHAMMKRGVAMDYWGGLVTVSS 142

DB 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

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QY 121 LPTV-----GLFTYWGGLVTVSS 139

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QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

QY 121 LPTV-----GLFTYWGGLVTVSS 139

DR InterPro: IPR007110; I9_1like.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003596; I9_MHC.
 DR Pfam: PF00047; I9_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS00835; I9_LIKE; 1.
 KW Plasmid.
 FT NON TER 121 121
 SQ SEQUENCE 121 AA; 13255 MW; D2934EBC6C59D5B CRC64;

Query Match 62.3%; Score 462.5; DB 11; Length 121;

Best Local Similarity 73.2%; Pred. No. 3e-41;

Matches 90; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 20 QVLOESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRP 79

DB 1 QVLOESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRP 79

QY 80 SALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP 139

DB 61 SALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP 117

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

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QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

QY 140 VSS 142

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:09 ; Search time 30.2434 Seconds
(without alignments)
745.259 Million cell updates/sec

Title: US-09-772-103-10
742
1 MAVLVFLCLVAFPSCVLSQ.....MKRGYANDYWGQGLTVTVSS 142

Sequence: BIOSUM62
Gapop 10.0 , Gapext 0.5

Scoring table: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: A_Geneseq_19Jun03:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	742	100.0	142	22	AA66523	Humanised anti-CTL
2	664	89.5	142	22	AA66520	Mouse antibody 26
3	632	85.2	140	23	ABP51940	Silenced anti-CD28
4	603.5	81.3	137	18	AAW30273	Heavy chain of Hum
5	545	73.5	140	18	AAW22538	Murine anti-human
6	545	73.5	140	23	AAE20201	Murine 44H104 mab
7	542	73.0	478	23	ABG31730	Murine m166 antibo
8	541.5	73.0	137	22	ABG31730	Ganglioside GD2 sp
9	530	71.4	151	17	AA98941	Humanised anti-CD3

10	529.5	71.4	135	8	AA670991	Sequence of the he
11	527.5	71.1	137	18	AAW30277	Heavy chain of MuM
12	527	71.0	138	17	AAW01146	Mab 10.1 heavy cha
13	525	70.8	119	17	AA98492	NEWM humanised 2b6
14	525	70.8	138	22	AA69656	Murine m166 antibo
15	522	70.4	119	19	AAW42471	NEWM humanised hea
16	518	69.8	138	18	AAW08942	Heavy chain variab
17	515.5	69.5	116	17	AAW05823	Humanised ID10 ant
18	515.5	69.5	273	17	AAW05827	Humanised ID10 ant
19	515.5	69.5	446	17	AAW05829	Humanised ID10 ant
20	515	69.4	138	18	AAW08944	Heavy chain variab
21	515	69.4	183	12	AAW15326	IL-2 chimeric antel
22	515	69.4	183	14	AAW32128	Anti-IL2R-alpha an
23	514	69.3	152	20	AAW49210	Mab 1A7 heavy chai
24	514	69.3	152	20	AAW28469	Heavy chain variab
25	514	69.3	152	20	AAW21546	Monoclonal antibod
26	514	69.3	263	20	AAW28470	Vh-(Lk)-Vl of anti
27	512.5	69.1	139	23	AAW79726	Anti-Streptococcus
28	509	68.6	152	17	AAW037200	Anti-Idiotypic mono
29	508	68.5	358	23	AAE27929	Human CH2 domain d
30	508	68.5	358	24	ABE82838	Antibody C5E10 CH2
31	508	68.5	468	23	AAE27928	Human C5E10 antibo
32	508	68.5	468	24	ABE82837	Antibody C5E10 hea
33	507.5	68.4	120	20	AAW22432	TM27 antibody VH c
34	507	68.3	144	17	AAW98944	Humanised anti-CD3
35	504.5	68.0	118	22	AAW81970	Ganglioside GD2 sp
36	504.5	68.0	120	20	AAW22429	TM27 antibody VH c
37	504.5	68.0	581	22	AAW81972	TM27 antibody VH c
38	503.5	67.9	120	20	AAW22431	Ganglioside GD2 sp
39	502.5	67.7	120	20	AAW22430	TM27 antibody VH c
40	498.5	67.2	133	18	AAW10546	Wild type murine a
41	497.5	67.0	120	20	AAW22433	TM27 antibody VH c
42	494.5	66.6	120	16	AAW77303	Variable heavy cha
43	494.5	66.6	193	23	ABP43199	Human ovarian anti
44	493.5	66.5	120	24	AAO16027	Cyclic bingle-stra
45	492.5	66.4	132	15	AAW53331	KM-603 heavy chain

ALIGNMENTS

RESULT 1	AA66523	standard; Protein; 142 AA.
ID	AA66523;	
AC	AA66523;	
XX		
DT	22-OCT-2001 (first entry)	
XX		
DE	Humanised anti-CTLA4 heavy chain.	
XX		
KW	Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;	
KW	immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;	
KW	T cell; humanised antibody; autoimmune disorder; graft rejection;	
KW	allergy; heavy chain.	
XX		
OS	Homo sapiens.	
OS	Mus musculus.	
OS	Synthetic.	
XX		
PN	WO200154732-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	26-JAN-2001; 2001WO-US02653.	
XX		
PR	27-JAN-2000; 2000US-0178473.	
XX		
PA	(GENY) GENETICS INST INC.	
XX		
PI	Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;	
XX	O'Hara D, Hinton P, Teurushita N;	
XX		

DR WPI: 2001.483195/52.
 DR N-PSDB; AAH76441, AAH76443.
 XX Novel antibody-toxic group conjugate comprising an antibody that
 PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response
 XX Claim 15; Fig 10; 123pp; English.

CC The invention relates to an antibody-toxic group conjugate comprising
 CC an antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is
 CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 CC The antibody of the invention is a humanised anti-CTLA4 antibody
 CC comprising a sequence of 128 or 142 amino acids fully defined in the
 CC specification. The antibody-toxic group conjugate is useful for
 CC modulating the immune response in a subject suffering from a disorder
 CC or condition such as autoimmune disorder, immune response to a graft,
 CC allergic response or an immune response to a therapeutic protein.
 CC The antibody is also useful for research purposes, e.g., in staining
 CC and isolating CTLA4-bearing cells. The antibody is also useful for
 CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
 CC fragments of the receptor, for vaccine preparation, and for determining
 CC the effectiveness of an agent to down-regulate CTLA4 activity. The
 CC present sequence is the heavy chain of humanised anti-CTLA4
 CC antibody.

XX Sequence 142 AA;

Query Match 100.0%; Score 742; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 8.1e-60;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVVLVFLCLVAFPSCVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTGYTWYRPP 60
 DB 1 MAVVLVFLCLVAFPSCVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTGYTWYRPP 60
 QY 61 GKGLFEMLVGIWAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 DB 61 GKGLFEMLVGIWAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 QY 121 AMMKRGYAMDYWGQGLTVTVSS 142
 DB 121 AMMKRGYAMDYWGQGLTVTVSS 142

RESULT 2
 AAG6520
 ID AAG6520 standard; Protein; 142 AA.

XX AAG6520;
 AC AAG6520;
 XX 22-OCT-2001 (first entry)

DE Mouse antibody 26 heavy chain variable region.

XX Mouse; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
 KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
 KW T cell; humanised antibody; autoimmune disorder; graft rejection;
 KW allergy; antibody 26; heavy chain variable region; VH.

XX Mus musculus.

XX WO200154732-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02653.

XX 27-JAN-2000; 2000US-0178473.

XX (GENY) GENETICS INST INC.

XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
 PI O'Hara D, Hinton P, Tsurushita N;
 XX WPI: 2001.483195/52.
 DR N-PSDB; AAH76438.

XX Novel antibody-toxic group conjugate comprising an antibody that
 PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response
 XX Example 7; Page 84; 123pp; English.

CC The invention relates to an antibody-toxic group conjugate comprising
 CC an antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is
 CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 CC The antibody of the invention is a humanised anti-CTLA4 antibody
 CC comprising a sequence of 128 or 142 amino acids fully defined in the
 CC specification. The antibody-toxic group conjugate is useful for
 CC modulating the immune response in a subject suffering from a disorder
 CC or condition such as autoimmune disorder, immune response to a graft,
 CC allergic response or an immune response to a therapeutic protein.
 CC The antibody is also useful for research purposes, e.g., in staining
 CC and isolating CTLA4-bearing cells. The antibody is also useful for
 CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
 CC fragments of the receptor, for vaccine preparation, and for determining
 CC the effectiveness of an agent to down-regulate CTLA4 activity. The
 CC present sequence is the heavy chain variable region of mouse
 CC antibody 26. It was used in the construction of the humanised anti-CTLA4
 CC antibody of the invention.

XX Sequence 142 AA;

Query Match 89.5%; Score 664; DB 22; Length 142;
 Best Local Similarity 88.0%; Pred. No. 9.8e-53;
 Matches 125; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAVVLVFLCLVAFPSCVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTGYTWYRPP 60
 DB 1 MDVLVFLCLVAFPSCVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTGYTWYRPP 60
 QY 61 GKGLFEMLVGIWAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 DB 61 GKGLFEMLVGIWAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 QY 121 AMMKRGYAMDYWGQGLTVTVSS 142
 DB 121 AMMKRGYAMDYWGQGLTVTVSS 142

RESULT 3
 ABP51940
 ID ABP51940 standard; Protein; 140 AA.

XX ABP51940;

AC ABP51940;
 XX 08-OCT-2002 (first entry)

DE Silenced anti-CD28 antibody heavy chain protein SEQ ID NO:6.

XX Silenced anti-CD28 antibody; mitogenic; immunosuppressive; antirheumatic;
 KW antirheumatic; antinflammatory; dermatological; neuroprotective; asthma;
 KW antidiabetic; antiallergic; T-cell tolerance inducer; myasthenia gravis;
 KW tissue transplant rejection; graft-versus host disease; type I diabetes;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; immune disease; immune reaction suppressor;
 KW atopic dermatitis.

XX Homo sapiens.
 OS Homo sapiens.
 OS Synthetic.

Tue Dec 2 07:00:55 2003

us-09-772-103-10.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:44:30 ; Search time 20.4503 Seconds
(without alignments)
1280.712 Million cell updates/sec

Title: US-09-772-103-10
Perfect score: 742
Sequence: 1 MAVVLFLCLVAFPSCVLSQ.....MKRGVANDYMGQTLVTVSS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	72.5	140	9	US-09-007-093-4
2	539.5	72.7	139	8	US-08-778-784-37
3	530	71.4	151	10	US-09-797-941A-2
4	527.5	71.1	135	8	US-08-779-784-32
5	525	70.8	119	15	US-10-144-644-62
6	522.5	70.4	135	12	US-10-010-729-68
7	514	69.3	152	10	US-09-990-205-4
8	514	69.3	152	15	US-10-153-401-4
9	514	69.3	263	15	US-10-153-401-66
10	512.5	69.1	139	9	US-09-881-823-4
11	511.5	68.9	141	15	US-10-207-655-359
12	507	68.3	144	10	US-09-797-941A-8
13	494.5	66.6	250	15	US-10-194-975-110
14	485	65.4	119	15	US-10-144-644-15
15	478	64.4	121	15	US-10-056-052-20

16	472	63.6	119	15	US-10-144-644-19	Sequence 19, Appl
17	471	63.5	119	15	US-10-153-401-16	Sequence 16, Appl
18	468	63.1	333	15	US-10-059-261-61	Sequence 61, Appl
19	466.5	62.9	120	15	US-10-194-975-112	Sequence 112, Appl
20	466	62.8	119	14	US-10-025-687-5	Sequence 5, Appl
21	466	62.8	119	15	US-10-125-687-5	Sequence 5, Appl
22	466	62.8	249	9	US-09-730-374-3	Sequence 3, Appl
23	463	62.4	119	15	US-10-232-187-2	Sequence 2, Appl
24	462.5	62.3	121	12	US-10-010-729-11	Sequence 11, Appl
25	461.5	62.2	116	12	US-10-169-351-108	Sequence 108, App
26	458.5	61.8	116	15	US-10-194-975-100	Sequence 100, App
27	458.5	61.8	487	9	US-09-800-729-145	Sequence 145, App
28	456	61.5	116	9	US-09-881-823-18	Sequence 18, Appl
29	453.5	61.1	112	9	US-09-824-286-3	Sequence 3, Appl
30	451	60.8	271	15	US-10-207-655-254	Sequence 254, App
31	451	60.8	556	15	US-10-207-655-268	Sequence 268, App
32	447.5	60.3	139	12	US-10-300-675-2	Sequence 2, Appl
33	447	60.2	121	15	US-10-207-655-252	Sequence 252, App
34	446.5	60.2	119	14	US-10-140-555-2	Sequence 2, Appl
35	444.5	59.9	126	15	US-10-067-800-68	Sequence 68, Appl
36	443	59.7	117	12	US-10-330-613-13	Sequence 13, Appl
37	443	59.7	117	12	US-10-330-530-13	Sequence 362, App
38	442.5	59.6	271	15	US-10-207-655-362	Sequence 363, App
39	442.5	59.6	505	15	US-10-207-655-363	Sequence 364, App
40	442.5	59.6	536	15	US-10-207-655-364	Sequence 35, Appl
41	442	59.6	580	12	US-10-310-719-35	Sequence 37, Appl
42	442	59.6	580	12	US-10-310-719-37	Sequence 360, App
43	438.5	59.1	122	15	US-10-207-655-360	Sequence 990, App
44	438	59.0	251	11	US-09-880-748-990	Sequence 1329, App
45	437.5	59.0	252	11	US-09-880-748-1329	

ALIGNMENTS

RESULT 1
US-09-007-093-4
Sequence 4, Application US/09007093
Patent No. US20020025315A1
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

... ..

[illegible]

MAVI VI PI CI VA EP SC TI SO VO I OE SC BC I VT PS

MAVI VI PI CI VA EP SC TI SO VO I OE SC BC I VT PS

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:40:15 ; Search time 10.9452 Seconds

(without alignments)
548.928 Million cell updates/sec

Title: US-09-772-103-10

Perfect score: 742

Sequence: 1 MAVLVFLGLVAFPSCVLSQ.....MKRGYANDYWGQGLTVTVSS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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19: /cgn2_6/ptodata/1/1aa/backfile14.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	603.5	81.3	137	2	US-08-621-751A-8
2	545	73.5	140	3	US-08-943-136-4
3	545	73.5	140	4	US-08-973-518-4
4	527.5	70.8	137	2	US-08-621-751A-4
5	525	70.8	137	1	US-08-667-769A-4
6	525	70.8	137	1	US-08-667-769A-62
7	525	70.8	138	1	PCT-US95-17082A-62
8	525	70.8	138	1	US-07-634-278-33
9	525	70.8	138	1	US-08-477-728-33
10	525	70.8	138	1	US-08-474-040-33
11	525	70.8	138	1	US-08-467-200-33
12	521	70.2	138	1	US-08-484-537-33
13	521	70.2	119	1	US-08-467-420A-62
14	521	70.2	119	1	US-08-940-110A-62
15	515.5	69.5	116	3	US-08-940-371-62
16	515.5	69.5	272	3	US-08-397-411-3
17	515.5	69.5	272	3	US-08-397-411-6
18	514	69.3	152	2	US-08-397-411-7
19	514	69.3	152	2	US-08-752-844-4
20	514	69.3	152	2	US-08-591-196-4
21	514	69.3	152	4	US-09-192-838B-4
22	514	69.3	152	4	US-09-293-533-4
23	514	69.3	152	4	US-09-324-191-4
24	514	69.3	263	2	US-08-752-844-66
25	507.5	68.4	120	2	US-09-293-533-66
26	507.5	68.4	120	3	US-08-652-558-8
27	504.5	68.0	120	2	US-09-254-189-5
					Sequence 4, Appl1

28	504.5	68.0	120	2	US-08-652-558-5	Sequence 5, Appl1
29	504.5	68.0	120	3	US-09-254-189-2	Sequence 2, Appl1
30	503.5	67.9	120	2	US-08-652-558-7	Sequence 7, Appl1
31	503.5	67.9	120	3	US-09-254-189-4	Sequence 4, Appl1
32	502.5	67.7	120	2	US-08-652-558-6	Sequence 6, Appl1
33	502.5	67.7	120	3	US-09-254-189-3	Sequence 3, Appl1
34	497.5	67.0	120	2	US-08-652-558-9	Sequence 9, Appl1
35	497.5	67.0	120	3	US-09-254-189-6	Sequence 6, Appl1
36	485.5	65.4	120	4	US-08-057-430A-26	Sequence 26, Appl1
37	485	65.4	119	1	US-08-667-769A-15	Sequence 15, Appl1
38	485	65.4	119	5	PCT-US95-17082A-15	Sequence 15, Appl1
39	482.5	65.0	120	2	US-08-353-372A-36	Sequence 36, Appl1
40	482	65.0	142	2	US-08-480-774A-2	Sequence 2, Appl1
41	481.5	64.9	473	3	US-09-049-672A-4	Sequence 4, Appl1
42	479.5	64.6	121	3	US-08-881-037-67	Sequence 67, Appl1
43	476	64.2	222	2	US-08-190-199A-67	Sequence 67, Appl1
44	476	64.2	235	2	US-08-190-199A-61	Sequence 61, Appl1
45	472.5	63.7	242	6	5455030-15	Patent No. 5455030

ALIGNMENTS

RESULT 1

US-08-621-751A-8

Sequence 8, Application US/08621751A

Patent No. 5882644

GENERAL INFORMATION:

APPLICANT: Chang, Chung N.

APPLICANT: Landolfi, Nicholas F.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSER: MORRISON & FOERSTER LLP

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,751A

FILING DATE: 22-MAR-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Leinhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 321152000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141 MRSN FOERS SFO

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-08-621-751A-8

Query Match 81.3%, Score 603.5, DB 2, Length 137;
Best local Similarity 83.1%, Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 14; Indels 5; Gaps 1;

1 MAVLVFLGLVAFPSCVLSQ.....MKRGYANDYWGQGLTVTVSS 142

Db 1 MAVLALVLCTVFPSCALSOVLOESGPGLVKPSSETLSLTCTVSGFSLTNTAINMWKOP 60
Qy 61 GKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTADTAVYCARGPPH 120
Db 61 GKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTADTAVYCARGPPH 116
Qy 121 AMMRGVADYWGQGTIVTVSS 142
Db 117 -TGTRGYFFDYWGQGTIVTVSS 137

RESULT 2

US-08-943-136-4
; Sequence 4, Application US/08943136
; Patent No. 6291208
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,136
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-943-136-4

Query Match 73.5%; Score 545; DB 3; Length 140;

Best Local Similarity 76.2%; Pred. No. 1.1e-48;

Matches 109; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

Qy 1 MAVLALVLCTVAFPPSC-VLSOVLOESGPGLVKPSQTLSTCTVSGFSLTSGVWVWROP 59
Db 1 MALVLVFLSLAFAFSCGVLSOVLOESGPGLVKPSQTLSTCTVSGFSLTSGVWVWROP 60
Qy 60 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTADTAVYCARGPP 119
Db 61 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTADTAVYCARGPP 120
Qy 120 HAMMRGVADYWGQGTIVTVSS 142
Db 117 -TGTRGYFFDYWGQGTIVTVSS 137

Db 121 DYV--HYAMDYWGQGTIVTVSS 140

RESULT 3

US-08-973-518-4
; Sequence 4, Application US/08973518
; Patent No. 6328962
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-973-518-4

Query Match 73.5%; Score 545; DB 4; Length 140;

Best Local Similarity 76.2%; Pred. No. 1.1e-48;

Matches 109; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

Qy 1 MAVLVLCTVAFPPSC-VLSOVLOESGPGLVKPSQTLSTCTVSGFSLTSGVWVWROP 59
Db 1 MALVLVFLSLAFAFSCGVLSOVLOESGPGLVKPSQTLSTCTVSGFSLTSGVWVWROP 60
Qy 60 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTADTAVYCARGPP 119
Db 61 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTADTAVYCARGPP 120
Qy 120 HAMMRGVADYWGQGTIVTVSS 142
Db 121 DYV--HYAMDYWGQGTIVTVSS 140
RESULT 4
US-08-621-751A-4
; Sequence 4, Application US/08621751A
; Patent No. 5882644
; GENERAL INFORMATION:
; APPLICANT: Chang, Chung N.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Martin, Ulrich
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE